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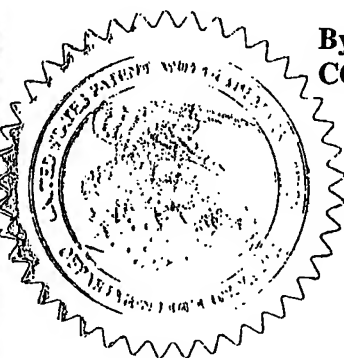
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Yocum, *et al.*Attorney
Docket No. BGI-152-3

For: Methods and Organisms for Production of B6 Vitamers

Commissioner for Patents
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Washington, D.C. 20231

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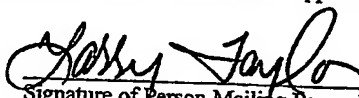
CERTIFICATION UNDER 37 CFR 1.10

Date of Deposit: March 29, 2002Mailing Label Number: EL 833 314 145 US

I hereby certify that this Cover Sheet for Filing Provisional Application (37 C.F.R. §1.51(2)(i)) and the documents referred to as attached therein are being deposited with the United States Postal Service on the date indicated above in an envelope as "Express Mail Post Office to Addressee" service under 37 CFR 1.10 and addressed to the Commissioner for Patents, Box Provisional Patent Application, Washington, D.C. 20231.

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COVER SHEET FOR FILING PROVISIONAL PATENT APPLICATION

Dear Sir:

The accompanying application, entitled "Methods and Organisms for Production of B6 Vitamers," is a provisional patent application under 37 C.F.R. §1.51(c) and §1.53(c).

1. ☒ The name(s) and address(es) of the inventor(s) of this application is/are as follows:

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2. ☒ The following documents are enclosed:

- ☒ 28 page(s) of Specification
- ☒ 6 page(s) of Claims
- ☒ 1 page(s) of Abstract
- ☒ 12 page(s) of Sequence Listing
- ☒ 7 sheets of Informal Drawings; and
- ☒ Return postcard.

3. ☒ The fee for filing this provisional application, as set forth in 37 CFR 1.16(k), is \$160.00.

- a. ☒ A check for this filing fee is enclosed.
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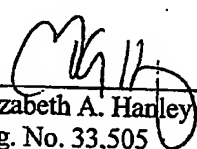
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METHODS AND ORGANISMS FOR PRODUCTION OF B6 VITAMERS

Background of the Invention

5 Vitamin B6, also known as pyridoxine or pyridoxol (PN), or one of a number of closely related compounds, is an essential dietary nutrient for most, if not all, animals, while many micro-organisms (bacteria, fungi, algae, etc.) and plants are capable of synthesizing their own vitamin B6 or compound(s) related to vitamin B6. When an animal ingests PN or a related compound that has vitamin B6 activity, the
10 compound is converted ultimately into pyridoxal phosphate (PLP) and/or pyridoxamine phosphate (PMP), which are the active forms of vitamin B6 in all living organisms. PLP acts as a cofactor for many important or essential enzymes in all living organisms, including transaminases, racemases, and decarboxylases. PLP and PMP are easily interconverted by ubiquitous transaminases.

15 Vitamin B6 is of commercial importance in vitamin pills, pharmaceutical applications, and as an animal feed additive that enhances growth or desirable growth characteristics in farm and domestic animals. The currently used commercial process for producing vitamin B6 is a synthetic chemical process. However, a fermentation process using a microorganism (see US Patent application No. 09/667,569, filed
20 September 21, 2000, hereby incorporated in its entirety by reference) or a biosynthetic process using a plant species can be more cost effective in the long run, and may be environmentally more attractive.

The biosynthetic pathway for PLP in *E. coli* has been elucidated (reviewed in Mittengruber, G., (2001) *J. Mol. Microbiol. Biotechnol.* 3(1): 1-20; Cane, D.E., et al. (2000) *J. Am. Chem. Soc.* 122: 4213-4214; Man, T-K, et al., (1996) *J. Bacteriol.* 178: 2445-2449). Enzymes encoded by the genes *epd*, *pdxB*, *pdxF*, and *pdxA* lead to synthesis of the precursor 1-hydroxy-3-amino acetone phosphate from erythrose-4-phosphate and glutamate. The enzyme encoded by *dxs* leads to the precursor 5'-deoxyxylulose phosphate from glycolytic intermediates. The enzyme encoded by *pdxJ*
30 then catalyzes the chemical coupling of the two precursors to give pyridoxol phosphate (also called pyridoxine phosphate or PNP). PNP is then oxidized to the active form, PLP, by the enzyme encoded by *pdxH*. This biosynthetic pathway to PLP in *E. coli*, as well as closely related pathways, are referred to herein as the Type A Pathway. Partially characterized mutants of *E. coli* have been described that produce about three- to seven-
35 fold more vitamin B₆-related compounds than the parent strain (Dempsey and Arcement (1971) *J. Bacteriol.* 107(2): 580-582). Partially characterized mutants of *B. subtilis* have been reported that produce 1 - 5 mg/l vitamin B₆, but it was not stated what level the

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parent strain produced (Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570). Notably, these organisms were not recombinantly produced.

A second biosynthetic pathway for vitamin B6, referred to herein as the Type B pathway, may exist in some organisms other than *E. coli* (Mittengruber, G.,
5 (2001) *J. Mol. Microbiol. Biotechnol.* 3(1):1-20). In particular, some fungi (for example from the genera *Cercospora*, *Neurospora*, *Aspergillus* and *Saccharomyces*), some bacteria (for example *B. subtilis* and *Staphylococcus aureus*), and all plants for which data exists do not contain any genes that are highly homologous to *E. coli* *pdxA* and *pdxJ*. Instead, these organisms contain genes that are homologous to *Cercospora* genes
10 named *SOR* (or *SNZ*) and *SNO*. In *Saccharomyces*, these homologs are called *PDX1* and *PDX2*, respectively, and in *B. subtilis*, these homologs are named *yaaD* and *yaaE*, respectively. In *B. subtilis*, there have been no reports as to whether *yaaD* or *yaaE* are actually involved in PLP biosynthesis. Protein or DNA sequence homology alone is not sufficient to establish biological function. For example, *B. subtilis* contains a gene,
15 *yhaF*, that encodes a protein that is significantly homologous to *E. coli* *pdxF*. However, when *yhaF* is mutated, the resulting mutant *B. subtilis* strain is a serine auxotroph, but not a PL auxotroph (see Example 3, below). Thus, the identification of a gene or genes involved in PLP biosynthesis in any given organism can not be done using sequence homology alone.

20 Results from ¹³C and ¹⁵N labeling studies suggest that the precursors that provide the carbon and nitrogen atoms in PL and related compounds are different in *E. coli* and *Saccharomyces cerevisiae* (Gupta, R., et al. (2001) *J. Am Chem. Soc.* 123: 11353-11359; Tayuza, K., et al. (1995) *Biochim. Biophys. Acta* 1244: 113-116.) However, the identity of the precursors for PL and related compounds in *S. cerevisiae* is
25 not yet known. Since most micro-organisms for which the entire genome sequence is known (for example *E. coli*, *S. cerevisiae* and *B. subtilis*) have either *pdxA* and *pdxJ* homologs or *SOR* and *SNO* homologs, but not both, it appears that most organisms that are capable of synthesizing PLP have either the well characterized Type A Pathway (for example *E. coli*, *Salmonella typhimurium*, and many other genera), or a distinctly
30 different and incompletely characterized pathway, e.g., the Type B Pathway. Specifically, members of the genera *Cercospora*, *Neurospora*, *Aspergillus*, *Saccharomyces*, *Bacillus*, *Arabidopsis*, and many other genera, appear to have a Type B pathway, and are lacking genes involved in the Type A Pathway. The intermediate compounds in the Type B Pathway have not yet been elucidated, although the final
35 product must be PLP (as for the Type A Pathway) or PMP, since these are the active forms of vitamin B6 in all known organisms.

Summary of the Invention

The present invention is based, at least in part, on the discovery of key enzyme-encoding genes of the B6 vitamer biosynthetic pathways in *Bacillus subtilis*. In particular, the invention is based, at least in part, on the discovery that the *yaaD* and *yaaE* genes of *B. subtilis* are required for B6 vitamer synthesis. Deletion of a portion of the *yaaD* and *yaaE* genes (which are adjacent in an operon, *e.g.*, the *yaaDE* operon) leads to PL auxotrophy. Overexpression of the *yaaDE* operon or the deregulation of the expression of the *yaaD* or *yaaE* genes leads to significantly increased production of B6 vitamers in, *e.g.*, *B. subtilis* strains. The *B. subtilis yaaDE* operon is required for pyridoxal phosphate (PLP) biosynthesis, an active form of vitamin B6 in all living organisms. The present invention describes that the expression of the *B. subtilis yaaDE* operon is a rate limiting step for production of compounds related to vitamin B6 in a wild type strain.

Accordingly, the present invention features methods of producing B6 vitamers, including, but not limited to, pyridoxine (or pyridoxol (PN)), pyridoxal (PL), pyridoxamine (PM), or the 5' phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP), using organisms in which the B6 vitamer pathway has been manipulated such that B6 vitamers are produced. Such methods include culturing a microorganism that overexpresses at least one B6 vitamer biosynthetic enzyme (*e.g.*, at least one of the *yaaD* or *yaaE* gene products), under conditions such that the B6 vitamer is produced. The production methods of the present invention further can include recovering the B6 vitamer.

The instant invention also features genetically modified organisms (*i.e.*, organisms that contain one or more modifications or mutations in the genome) that are capable of producing significantly more of a B6 vitamer than an unmodified parent organism. In particular, this invention features micro-organisms (including, for example, but not limited to, bacteria, yeasts, fungi, and algae) or macro-organisms such as plants that, when genetically modified, produce an increased amount, *e.g.*, at least about 10-fold more of a B6 vitamer, than the unmodified parent organism. Specific examples are given herein in which *Bacillus subtilis* and *Escherichia coli* strains have been genetically modified such that they produce significant amounts of a B6 vitamer. Accordingly, the present invention features organisms that have been genetically modified to increase the activity of one or more enzymes that catalyze(s) a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism.

Yet another aspect of the invention features recombinant microorganisms which overexpress at least one *Bacillus* (*e.g.*, *B. subtilis*) B6 vitamer biosynthetic

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enzyme (e.g., at least one of the *yaaD* or *yaaE* gene products) are described. In one embodiment, the recombinant microorganism is Gram positive (e.g., microorganisms belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*). In another embodiment, the recombinant microorganism is Gram negative. Particularly preferred is a *Bacillus* recombinant microorganism (e.g., *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Bacillus pumilus*, *Bacillus halodurans*, and the like).

Recombinant vectors that contain genes encoding *Bacillus* B6 vitamers biosynthetic enzymes, e.g., *yaaD* or *yaaE* genes, are also described.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Brief Description of the Drawings

Figure 1 depicts the chemical structures of vitamin B6 and related compounds.

Figure 2 depicts the biosynthetic pathway for PLP in *E. coli*.

Figure 3 depicts the standard curves generated by *Saccharomyces unarum* strain ATCC 9080 after feeding serial dilutions of PN, PL, and PM (as described in Example 1).

Figure 4 is a schematic representation of the plasmid pDX1F.

Figure 5 is a schematic representation of the plasmid pDX11F.

Figure 6 is a schematic representation of the plasmid pDX14R.

Figure 7 is a schematic representation of the plasmid pDX17R.

Detailed Description of the Invention

The present invention is based, at least in part, on the identification of *Bacillus* (e.g., *B. subtilis*) genes that encode essential enzymes of the B6 vitamers biosynthetic pathway. In particular, the present invention features methods based on manipulation of the B6 vitamers biosynthetic pathway in a microorganism such that certain desirable compounds are produced.

In particular, the invention is based, at least in part, on the discovery that the *yaaD* and *yaaE* genes of *B. subtilis* are required for B6 vitamers synthesis, including, but not limited to, pyridoxine (or pyridoxol (PN)), pyridoxal (PL), pyridoxamine (PM), or the 5' phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP). The *yaaD* and *yaaE* genes are adjacent on an operon, e.g., the *yaaDE* operon. The *yaaD* and *yaaE* genes encode the YaaD and YaaE proteins,

respectively. Overexpression of the *yaaDE* operon with a strong constitutive promoter or the deregulation of the expression of the *yaaD* or *yaaE* gene(s) leads to significantly increased production of B6 vitamers. These quantities are significantly higher relative to the associated parent strains than those reported in previous studies, which have
5 employed mutant *E. coli* strains (Dempsey and Arcement (1971) *J. Bacteriol.* 107 (2): 580-582), or mutant *B. subtilis* strains (Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570).

Accordingly, the present invention features organisms that have been genetically modified to increase the activity of one or more enzymes that catalyze a step
10 in the biosynthesis of a B6 vitamer, such that B6 vitamer production from the modified organism is increased compared to B6 production in an unmodified parent organism. In one embodiment, B6 vitamer production is at least ten-fold higher than from the unmodified parent organism. In another embodiment, the organism is genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step
15 in the biosynthesis of a B6 vitamer, e.g., *yaaD* or *yaaE*. The organism may be, for example, *B. subtilis*.

The present invention also features methods of producing a B6 vitamer comprising culturing a microorganism that has been genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a
20 B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism, under conditions such that the B6 vitamer is produced. The B6 vitamer may then be subsequently recovered. Overproduction of the rate limiting enzyme for B6 vitamer production in any organism that is capable of producing B6 vitamers will lead to overproduction of B6 vitamers.

The terms "B6 vitamer" or "B6 vitamers," as used herein, shall refer to any compound or mixture of compounds that has any biological activity in any biological assay for vitamin B6. B6 vitamers include, but are not limited to, pyridoxine (also called pyridoxol or PN), pyridoxal (PL), pyridoxamine (PM), the 5'
25 phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP), and any derivative or related compound that can be converted to the active forms (PLP or PMP) in a test organism. Thus, for example, the acetate esters or other esters of any of the available hydroxyl groups of any of the aforementioned six compounds, and which are likely to be hydrolyzed by specific or non-specific esterases, are included in B6 vitamers. Also, various salts, such as hydrochloride salts, of any of
30 the aforementioned compounds are included in B6 vitamers.

The term "B6 vitamer biosynthetic pathway" includes the biosynthetic pathway involving B6 vitamer biosynthetic enzymes (e.g., polypeptides encoded by

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biosynthetic enzyme-encoding genes), compounds (*e.g.*, precursors, substrates, intermediates or products), cofactors and the like utilized in the formation or synthesis of B6 vitamers. The term "B6 vitamer biosynthetic pathway" includes the biosynthetic pathway leading to the synthesis of B6 vitamers in a microorganism (*e.g.*, *in vivo*) as well as the biosynthetic pathway leading to the synthesis of B6 vitamers *in vitro*.

A "biological assay for a B6 vitamer" includes, for example, any assay that is capable of quantifying B6 vitamer activity by measuring growth of an organism that requires the feeding of a B6 vitamer (*i.e.*, a compound that the fed organism can convert into PLP or PMP) for growth. Samples to be assayed are diluted serially in an appropriate medium and fed to the appropriate organism. Standard curves are generated by serially diluting known amounts of PL, PN, or PM, and feeding these dilutions to the test organism. By comparing dilutions of the unknown samples to the standard curves, total B6 vitamer activity can be determined, for example as PL equivalents if PL was used to generate the standard curve.

Various aspects of the invention are described in further detail in the following subsections.

I. Genes Encoding Various B6 Vitamer Biosynthetic Enzymes

In one embodiment, the present invention features targeting or modifying various biosynthetic genes or enzymes of the B6 vitamer biosynthetic pathway. In particular, the invention features modifying various enzymatic activities associated with said pathways by modifying or altering the genes encoding said biosynthetic enzymes.

The term "gene", as used herein, includes a nucleic acid molecule (*e.g.*, a DNA molecule or segment thereof) that, in an organism, can be separated from another gene or other genes, by intergenic DNA (*i.e.*, intervening or spacer DNA which naturally flanks the gene and/or separates genes in the chromosomal DNA of the organism). Alternatively, a gene may slightly overlap another gene (*e.g.*, the 3' end of a first gene overlapping the 5' end of a second gene), said overlapping genes separated from other genes by intergenic DNA. A gene may direct synthesis of an enzyme or other protein molecule (*e.g.*, may comprise coding sequences, for example, a contiguous open reading frame (ORF) which encodes a protein) or may itself be functional in the organism. A gene in an organism, may be clustered in an operon, as defined herein, said operon being separated from other genes and/or operons by the intergenic DNA. An "isolated gene", as used herein, includes a gene which is essentially free of sequences which naturally flank the gene in the chromosomal DNA of the organism from which the gene is derived (*i.e.*, is free of adjacent coding sequences which encode a second or

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distinct protein, adjacent structural sequences or the like) and optionally includes 5' and 3' regulatory sequences, for example promoter sequences and/or terminator sequences. In one embodiment, an isolated gene includes predominantly coding sequences for a protein (e.g., sequences which encode *Bacillus* proteins). In another embodiment, an isolated gene includes coding sequences for a protein (e.g., for a *Bacillus* protein) and adjacent 5' and/or 3' regulatory sequences from the chromosomal DNA of the organism from which the gene is derived (e.g., adjacent 5' and/or 3' *Bacillus* regulatory sequences). Preferably, an isolated gene contains less than about 10 kb, 5 kb, 2 kb, 1 kb, 0.5 kb, 0.2 kb, 0.1 kb, 50 bp, 25 bp or 10 bp of nucleotide sequences that naturally flank the gene in the chromosomal DNA of the organism from which the gene is derived.

The term "operon" includes at least two adjacent genes or ORFs, optionally overlapping in sequence at either the 5' or 3' end of at least one gene or ORF. The term "operon" includes a coordinated unit of gene expression that contains a promoter and possibly a regulatory element associated with one or more adjacent genes or ORFs (e.g., structural genes encoding enzymes, for example, biosynthetic enzymes). Expression of the genes (e.g., structural genes) can be coordinately regulated, for example, by regulatory proteins binding to the regulatory element or by anti-termination of transcription. The genes of an operon (e.g., structural genes) can be transcribed to give a single mRNA that encodes all of the proteins.

A "gene having a mutation" or "mutant gene" as used herein, includes a gene having a nucleotide sequence which includes at least one alteration (e.g., substitution, insertion, deletion) such that the polypeptide or protein encoded by said mutant exhibits an activity that differs from the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. In one embodiment, a gene having a mutation or mutant gene encodes a polypeptide or protein having an increased activity as compared to the polypeptide or protein encoded by the wild-type gene, for example, when assayed under similar conditions (e.g., assayed in microorganisms cultured at the same temperature). As used herein, an "increased activity" or "increased enzymatic activity" is one that is at least 5% greater than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene, preferably at least 5-10% greater, more preferably at least 10-25% greater and even more preferably at least 25-50%, 50-75% or 75-100% greater than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Ranges intermediate to the above-recited values, e.g., 75-85%, 85-90%, 90-95%, are also intended to be encompassed by the present invention. As used herein, an "increased activity" or "increased enzymatic activity" can also include an activity that is at least 1.25-fold greater than the activity of the polypeptide or protein encoded by the wild-type gene, preferably at least 1.5-fold

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greater, more preferably at least 2-fold greater and even more preferably at least 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or greater than the activity of the polypeptide or protein encoded by the wild-type gene.

In another embodiment, a gene having a mutation or mutant gene encodes a polypeptide or protein having a reduced activity as compared to the polypeptide or protein encoded by the wild-type gene, for example, when assayed under similar conditions (*e.g.*, assayed in microorganisms cultured at the same temperature). A mutant gene also can encode no polypeptide or have a reduced level of production of the wild-type polypeptide. As used herein, a "reduced activity" or "reduced enzymatic activity" is one that is at least 5% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene, preferably at least 5-10% less, more preferably at least 10-25% less and even more preferably at least 25-50%, 50-75% or 75-100% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Ranges intermediate to the above-recited values, *e.g.*, 75-85%, 85-90%, 90-95%, are also intended to be encompassed by the present invention. As used herein, a "reduced activity" or "reduced enzymatic activity" can also include an activity that has been deleted or "knocked out" (*e.g.*, approximately 100% less activity than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene).

Activity can be determined according to any well accepted assay for measuring activity of a particular protein of interest. Activity can be measured or assayed directly, for example, measuring an enzymatic or biological activity of a protein isolated or purified from a cell or microorganism. Alternatively, an activity can be measured or assayed within a cell or microorganism or in an extracellular medium. For example, assaying for a mutant gene (*i.e.*, said mutant encoding a reduced enzymatic activity) can be accomplished by expressing the mutated gene in a microorganism, for example, a mutant microorganism in which the enzyme is temperature-sensitive, and assaying the mutant gene for the ability to complement a temperature sensitive (T_s) mutant for enzymatic activity. A mutant gene that encodes an "increased enzymatic activity" can be one that complements the T_s mutant more effectively than, for example, a corresponding wild-type gene. A mutant gene that encodes a "reduced enzymatic activity" is one that complements the T_s mutant less effectively than, for example, a corresponding wild-type gene.

It will be appreciated by the skilled artisan that even a single substitution in a nucleic acid or gene sequence (e.g., a base substitution that encodes an amino acid change in the corresponding amino acid sequence) can dramatically affect the activity of an encoded polypeptide or protein as compared to the corresponding wild-type

polypeptide or protein. A mutant gene (e.g., encoding a mutant polypeptide or protein), as defined herein, is readily distinguishable from a nucleic acid or gene encoding a protein homologue in that a mutant gene encodes a protein or polypeptide having an altered activity, optionally observable as a different or distinct phenotype in a

5 microorganism expressing said mutant gene or producing said mutant protein or polypeptide (i.e., a mutant microorganism) as compared to a corresponding microorganism expressing the wild-type gene. By contrast, a protein homologue has an identical or substantially similar activity, optionally phenotypically indiscernible when produced in a microorganism, as compared to a corresponding microorganism

10 expressing the wild-type gene. Accordingly it is not, for example, the degree of sequence identity between nucleic acid molecules, genes, protein or polypeptides that serves to distinguish between homologues and mutants, rather it is the activity of the encoded protein or polypeptide that distinguishes between homologues and mutants: homologues having, for example, low (e.g., 30-50% sequence identity) sequence

15 identity yet having substantially equivalent functional activities, and mutants, for example sharing 99% sequence identity yet having dramatically different or altered functional activities.

In a preferred embodiment, the genes of the present invention are derived from *Bacillus*. The term "derived from *Bacillus*" or "*Bacillus*-derived" includes a gene

20 which is naturally found in microorganisms of the genus *Bacillus*. In another preferred embodiment, the genes of the present invention are derived from a microorganism selected from the group consisting of *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus*

25 *megaterium*, *Bacillus pumilus*, *Bacillus thuringiensis*, *Bacillus halodurans*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type. In another preferred embodiment, the gene is derived from *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the genes of the present invention are derived from a microorganism selected from the group consisting of

30 *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, and *Bacillus pumilus*. In a particularly preferred embodiment, the gene is derived from *Bacillus subtilis* (e.g., is *Bacillus subtilis*-derived). The term "derived from *Bacillus subtilis*" or "*Bacillus subtilis*-derived" includes a gene which is naturally found in the microorganism *Bacillus subtilis*. Included within the scope of the present invention are

35 *Bacillus*-derived genes (e.g., *B. subtilis*-derived genes), for example, *Bacillus* or *B. subtilis yaaD* or *yaaE* genes.

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II. Recombinant Nucleic Acid Molecules and Vectors

The present invention further features recombinant nucleic acid molecules (*e.g.*, recombinant DNA molecules) that include genes described herein (*e.g.*, isolated genes), preferably *Bacillus* genes, more preferably *Bacillus subtilis* genes, even more preferably *Bacillus subtilis* B6 vitamer biosynthetic genes. The term "recombinant nucleic acid molecule" includes an isolated nucleic acid molecule (*e.g.*, a DNA molecule) that has been altered, modified or engineered such that it differs in nucleotide sequence from the native or natural nucleic acid molecule from which the recombinant nucleic acid molecule was derived (*e.g.*, by addition, deletion or substitution of one or more nucleotides). Preferably, a recombinant nucleic acid molecule (*e.g.*, a recombinant DNA molecule) includes an isolated gene of the present invention operably linked to regulatory sequences. The phrase "operably linked to regulatory sequence(s)" means that the nucleotide sequence of the gene of interest is linked to the regulatory sequence(s) in a manner which allows for expression (*e.g.*, enhanced, increased, constitutive, basal, attenuated, decreased or repressed expression) of the gene, preferably expression of a gene product encoded by the gene (*e.g.*, when the recombinant nucleic acid molecule is included in a recombinant vector, as defined herein, and is introduced into a microorganism). A "recombinant organism" is any organism that contains a recombinant nucleic acid molecule.

The term "regulatory sequence" includes nucleic acid sequences that affect (*e.g.*, modulate or regulate) expression of other nucleic acid sequences (*i.e.*, genes). In one embodiment, a regulatory sequence is included in a recombinant nucleic acid molecule in a similar or identical position and/or orientation relative to a particular gene of interest as is observed for the regulatory sequence and gene of interest as it appears in nature, *e.g.*, in a native position and/or orientation. For example, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence which accompanies or is adjacent to the gene of interest in the natural organism (*e.g.*, operably linked to "native" regulatory sequences (*e.g.*, to the "native" promoter). Alternatively, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence which accompanies or is adjacent to another (*e.g.*, a different) gene in the natural organism. Alternatively, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence from another organism. For example, regulatory sequences from other microbes (*e.g.*, other bacterial regulatory sequences, bacteriophage regulatory sequences and the like) can be operably linked to a particular gene of interest.

In one embodiment, a regulatory sequence is a non-native or non-naturally-occurring sequence (*e.g.*, a sequence which has been modified, mutated,

substituted, derivatized, deleted including sequences which are chemically synthesized). Preferred regulatory sequences include promoters, enhancers, termination signals, anti-termination signals, ribosome binding sites and other expression control elements (e.g., sequences to which repressors or inducers bind and/or binding sites for transcriptional and/or translational regulatory proteins, for example, in the transcribed mRNA). Such regulatory sequences are described, for example, in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in a microorganism (e.g., constitutive promoters and strong constitutive promoters), those which direct inducible expression of a nucleotide sequence in a microorganism (e.g., inducible promoters, for example, xylose inducible promoters) and those which attenuate or repress expression of a nucleotide sequence in a microorganism (e.g., attenuation signals or repressor sequences). It is also within the scope of the present invention to regulate expression of a gene of interest by removing or deleting regulatory sequences. For example, sequences involved in the negative regulation of transcription can be removed such that expression of a gene of interest is enhanced.

In one embodiment, a recombinant nucleic acid molecule of the present invention includes a nucleic acid sequence or gene that encodes at least one bacterial gene product (e.g., a B6 vitamer biosynthetic enzyme, e.g., the gene product of *yaaD* and/or *yaaE*) operably linked to a promoter or promoter sequence. Preferred promoters of the present invention include *Bacillus* promoters and/or bacteriophage promoters (e.g., bacteriophage which infect *Bacillus*). In one embodiment, a promoter is a *Bacillus* promoter, preferably a strong *Bacillus* promoter (e.g., a promoter associated with a biochemical housekeeping gene in *Bacillus* or a promoter associated with a glycolytic pathway gene in *Bacillus*). In another embodiment, a promoter is a bacteriophage promoter. In a preferred embodiment, the promoter is from the bacteriophage SP01. In a particularly preferred embodiment, a promoter is selected from the group consisting of *P₁₅*, *P₂₆*, or *P_{veg}* having for example, the following respective sequences:

30 GCTATTGACGACAGCTATGGTTCACTGTCCACCAACCAAACTGTGCTCAGT
ACCGCCAATATTTCTCCCTTGAGGGGTACAAAGAGGTGTCCCTAGAAGAGAT
CCACGCTGTGTAAAAATTTACAAAAAGGTATTGACTTTCCCTACAGGGTGT
GTAATAATTTAATTACAGGCGGGGGCAACCCCGCCTGT (SEQ ID NO:9),
GCCTACCTAGCTTCCAAGAAAGATATCCTAACAGCACAAGAGCGGAAAGAT
35 GTTTTGTCTACATCCAGAACAACCTCTGCTAAAATTCCTGAAAAATTTTGC
AAAAAGTTGTTGACTTTATCTACAAGGTGTGGTATAATAATCTTAACAACAG
CAGGACGC (SEQ ID NO:10); and

GAGGAATCATAGAATTTTGTCAAAATAATTTTATTGACAACGTCTTATTAAC
 GTTGATATAATTTAAATTTTATTGACAAAAATGGGCTCGTGTGTACAATA
 AATGTAGTGAGGTGGATGCAATG (SEQ ID NO:11). Additional preferred

promoters include *tef* (the translational elongation factor (TEF) promoter) and *pyc* (the
 5 pyruvate carboxylase (PYC) promoter), which promote high level expression in *Bacillus*
(e.g., Bacillus subtilis). Additional preferred promoters, for example, for use in Gram
 positive microorganisms include, but are not limited to, *amy* and SPO2 promoters.
 Additional preferred promoters, for example, for use in Gram negative microorganisms
 include, but are not limited to, *tac*, *trp*, *tet*, *trp-tet*, *lpp*, *lac*, *lpp-lac*, *lacIQ*, T7, T5, T3,
 10 *gal*, *trc*, *ara*, SP6, λ -PR or λ -PL.

In another embodiment, a recombinant nucleic acid molecule of the
 present invention includes a terminator sequence or terminator sequences (*e.g.*,
 transcription terminator sequences). The term "terminator sequences" includes
 regulatory sequences that serve to terminate transcription of mRNA. Terminator
 15 sequences (or tandem transcription terminators) can further serve to stabilize mRNA
(e.g., by adding structure to mRNA), for example, against nucleases.

In yet another embodiment, a recombinant nucleic acid molecule of the
 present invention includes sequences which allow for detection of the vector containing
 said sequences (*i.e.*, detectable and/or selectable markers), for example, genes that
 20 encode antibiotic resistance or sequences that overcome auxotrophic mutations, for
 example, *trpC*, fluorescent markers, drug markers, and/or colorimetric markers (*e.g.*,
lacZ/ β -galactosidase). In yet another embodiment, a recombinant nucleic acid molecule
 of the present invention includes an artificial ribosome binding site (RBS) or a sequence
 that becomes transcribed into an artificial RBS. The term "artificial ribosome binding
 25 site (RBS)" includes a site within an mRNA molecule (*e.g.*, coded within DNA) to
 which a ribosome binds (*e.g.*, to initiate translation) which differs from a native RBS
(e.g., a RBS found in a naturally-occurring gene) by at least one nucleotide. Preferred
 artificial RBSs include about 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22,
 23-24, 25-26, 27-28, 29-30 or more nucleotides of which about 1-2, 3-4, 5-6, 7-8, 9-10,
 30 11-12, 13-15 or more differ from the native RBS (*e.g.*, the native RBS of a gene of
 interest, for example, the native *yaaD* RBS

GAAATCATATAACTATACCTTGATTAGGGGGACCAAGAAATG
 (SEQ ID NO:12) or the native *yaaE* RBS
 CAAGAACGCGGCTGGTAAGAACATAGGAGCGCTGCTGACATG (SEQ ID
 35 NO:13)).

Preferably, nucleotides that differ are substituted such that they are
 identical to one or more nucleotides of an ideal RBS when optimally aligned for

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comparisons. Artificial RBSs can be used to replace the naturally-occurring or native RBSs associated with a particular gene. Artificial RBSs preferably increase translation of a particular gene. Preferred artificial RBSs (e.g., RBSs for increasing the translation of *yaaE*, for example, of *B. subtilis*) are set forth in Table 1, below.

Table 1: Preferred Ribosome Binding Sites

	10	20	
10			SEQ ID NO:
Native_yaaD	---GAAATCATATAACTATACCTTGATTAGGGGGGACC-	AAGAAATG	12
Native_yaaE	CAAGAACGCGGCTGGTAAGAACAT---	AGGAGCGCTGCTGACATG	13
IDEAL_RBS	-----TCTAGAAAGG----	AGGTG-----A-----	14
RBS1	-----TCTAGAAAGG----	AGGAG-----AAAACATG	15
15 RBS2	-----TCTAGAGG----	AGGAG-----AAAACATG	16
RBS101	-----TAAGAACAA----	AGGAGGAGAGCTGACATG	17
RBS103	-----TAAGAAGAA----	AGGAGGTGAGCTGACATG	18
RBS102	-----TAAGAACAG----	AGGAGGAGAGCTGACATG	19

20 The present invention further features vectors (e.g., recombinant vectors) that include nucleic acid molecules (e.g., genes or recombinant nucleic acid molecules comprising said genes) as described herein. The term "recombinant vector" includes a vector (e.g., plasmid, phage, phasmid, virus, cosmid or other purified nucleic acid vector) that has been altered, modified or engineered such that it contains greater, fewer or different nucleic acid sequences than those included in the native or natural nucleic acid molecule from which the recombinant vector was derived. Preferably, the recombinant vector includes a biosynthetic enzyme-encoding gene or recombinant nucleic acid molecule including said gene, operably linked to regulatory sequences, for example, promoter sequences, terminator sequences and/or artificial ribosome binding sites (RBSs), as defined herein. In another embodiment, a recombinant vector of the present invention includes sequences that enhance replication in bacteria (e.g., replication-enhancing sequences). In one embodiment, replication-enhancing sequences are derived from *E. coli*. In another embodiment, replication-enhancing sequences are derived from pBR322. In another embodiment, replication-enhancing sequences are derived from pSC101.

35 In yet another embodiment, a recombinant vector of the present invention includes antibiotic resistance sequences. The term "antibiotic resistance sequences" includes sequences which promote or confer resistance to antibiotics on the host organism (e.g., *Bacillus*). In one embodiment, the antibiotic resistance sequences are selected from the group consisting of *cat* (chloramphenicol resistance) sequences, *tet* (tetracycline resistance) sequences, *erm* (erythromycin resistance) sequences, *neo*

(neomycin resistance) sequences, *kan* (kanamycin resistance) and *spec* (spectinomycin resistance) sequences. Recombinant vectors of the present invention can further include homologous recombination sequences (e.g., sequences designed to allow recombination of the gene of interest into the chromosome of the host organism). For example, *bpr*, *vpr*, and/or *amyE* sequences can be used as homology targets for recombination into the host chromosome. It will further be appreciated by one of skill in the art that the design of a vector can be tailored depending on such factors as the choice of microorganism to be genetically engineered, the level of expression of gene product desired and the like.

III. Recombinant Microorganisms

The present invention further features microorganisms, i.e., recombinant microorganisms, that include vectors or genes (e.g., wild-type and/or mutated genes) as described herein. As used herein, the term "recombinant microorganism" includes a microorganism (e.g., bacteria, yeast cell, fungal cell, etc.) that has been genetically altered, modified or engineered (e.g., genetically engineered) such that it exhibits an altered, modified or different genotype and/or phenotype (e.g., when the genetic modification affects coding nucleic acid sequences of the microorganism) as compared to the naturally-occurring microorganism from which it was derived.

In one embodiment, a recombinant microorganism of the present invention is a Gram positive organism (e.g., a microorganism which retains basic dye, for example, crystal violet, due to the presence of a Gram-positive wall surrounding the microorganism). In a preferred embodiment, the recombinant microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*. In a more preferred embodiment, the recombinant microorganism is of the genus *Bacillus*. In another preferred embodiment, the recombinant microorganism is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus thuringiensis*, *Bacillus halodurans*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type. In another preferred embodiment, the recombinant microorganism is *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the recombinant microorganism is selected from the group consisting of *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, and *Bacillus pumilus*.

In another embodiment, the recombinant microorganism is a Gram negative (excludes basic dye) organism. In a preferred embodiment, the recombinant

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microorganism is a microorganism belonging to a genus selected from the group consisting of *Salmonella*, *Escherichia*, *Klebsiella*, *Serratia*, and *Proteus*. In a more preferred embodiment, the recombinant microorganism is of the genus *Escherichia*. In an even more preferred embodiment, the recombinant microorganism is *Escherichia coli*. In another embodiment, the recombinant microorganism is *Saccharomyces* (e.g., *S. cerevisiae*).

5 A preferred "recombinant" microorganism of the present invention is a microorganism having a deregulated B6 vitamer biosynthesis pathway or enzyme. The term "deregulated" or "deregulation" includes the alteration or modification of at least
10 one gene in a microorganism that encodes an enzyme in a biosynthetic pathway, such that the level or activity of the biosynthetic enzyme in the microorganism is altered or modified. Preferably, at least one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the gene product is enhanced or increased. The phrase "deregulated pathway" can also include a biosynthetic pathway in which more
15 than one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the level or activity of more than one biosynthetic enzyme is altered or modified. The ability to "deregulate" a pathway (e.g., to simultaneously deregulate more than one gene in a given biosynthetic pathway) in a microorganism in some cases arises from the particular phenomenon of microorganisms in which more than one
20 enzyme (e.g., two or three biosynthetic enzymes) are encoded by genes occurring adjacent to one another on a contiguous piece of genetic material termed an "operon" (defined herein). Due to the coordinated regulation of genes included in an operon, alteration or modification of the single promoter and/or regulatory element can result in alteration or modification of the expression of more than one gene product encoded by
25 the operon. Alteration or modification of the regulatory element can include, but is not limited to removing the endogenous promoter and/or regulatory element(s), adding strong promoters, inducible promoters or multiple promoters or removing regulatory sequences such that expression of the gene products is modified, modifying the chromosomal location of the operon, altering nucleic acid sequences adjacent to the
30 operon or within the operon such as a ribosome binding site, increasing the copy number of the operon, modifying proteins (e.g., regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of the operon and/or translation of the gene products of the operon, or any other conventional means of deregulating expression of genes routine in the art (including but not limited to use of
35 antisense nucleic acid molecules, for example, to block expression of repressor proteins). Deregulation can also involve altering the coding region of one or more genes

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to yield, for example, an enzyme that is feedback resistant or has a higher or lower specific activity.

In another preferred embodiment, a recombinant microorganism is designed or engineered such that at least one B6 vitamer biosynthetic enzyme, is overexpressed. The term "overexpressed" or "overexpression" includes expression of a gene product (e.g., a biosynthetic enzyme) at a level greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. In one embodiment, the microorganism can be genetically designed or engineered to overexpress a level of gene product greater than that expressed in a comparable microorganism which has not been engineered.

Genetic engineering can include, but is not limited to, altering or modifying regulatory sequences or sites associated with expression of a particular gene (e.g., by adding strong promoters, inducible promoters or multiple promoters or by removing regulatory sequences such that expression is constitutive), modifying the chromosomal location of a particular gene, altering nucleic acid sequences adjacent to a particular gene such as a ribosome binding site, increasing the copy number of a particular gene, modifying proteins (e.g., regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of a particular gene and/or translation of a particular gene product, or any other conventional means of deregulating expression of a particular gene routine in the art (including but not limited to use of antisense nucleic acid molecules, for example, to block expression of repressor proteins). Genetic engineering can also include deletion of a gene, for example, to block a pathway or to remove a repressor. In embodiments featuring microorganisms having deleted genes, the skilled artisan will appreciate that at least low levels of certain compounds may be required to be present in or added to the culture medium in order that the viability of the microorganism is not compromised. Often, such low levels are present in complex culture media as routinely formulated. Moreover, in processes featuring culturing microorganisms having deleted genes cultured under conditions such that commercially or industrially attractive quantities of product are produced, it may be necessary to supplement culture media with slightly increased levels of certain compounds.

In another embodiment, the microorganism can be physically or environmentally manipulated to overexpress a level of gene product greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. For example, a microorganism can be treated with or cultured in the presence of an agent known or suspected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription

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and/or translation are enhanced or increased. Alternatively, a microorganism can be cultured at a temperature selected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription and/or translation are enhanced or increased.

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IV: Culturing and Fermenting Recombinant Microorganisms

The term "culturing" includes maintaining and/or growing a living microorganism of the present invention (e.g., maintaining and/or growing a culture or strain). In one embodiment, a microorganism of the invention is cultured in liquid media. In another embodiment, a microorganism of the invention is cultured in solid media or semi-solid media. In a preferred embodiment, a microorganism of the invention is cultured in media (e.g., a sterile, liquid media) comprising nutrients essential or beneficial to the maintenance and/or growth of the microorganism (e.g., carbon sources or carbon substrate, for example carbohydrate, hydrocarbons, oils, fats, fatty acids, organic acids, and alcohols; nitrogen sources, for example, peptone, yeast extracts, meat extracts, malt extracts, soy flour, urea, ammonium sulfate, ammonium chloride, ammonium nitrate and ammonium phosphate; phosphorus sources, for example, phosphoric acid, sodium and potassium salts thereof; trace elements, for example, magnesium, iron, manganese, calcium, copper, zinc, boron, molybdenum, and/or cobalt salts; as well as growth factors such as amino acids, vitamins, and the like).

Preferably, microorganisms of the present invention are cultured under controlled pH. The term "controlled pH" includes any pH which results in production of the desired product. In one embodiment microorganisms are cultured at a pH of about 7. In another embodiment, microorganisms are cultured at a pH of between 6.0 and 8.5. The desired pH may be maintained by any number of methods known to those skilled in the art.

Also preferably, microorganisms of the present invention are cultured under controlled aeration. The term "controlled aeration" includes sufficient aeration (e.g., oxygen) to result in production of the desired product. In one embodiment, aeration is controlled by regulating oxygen levels in the culture, for example, by regulating the amount of oxygen dissolved in culture media. Preferably, aeration of the culture is controlled by agitating the culture. Agitation may be provided by a propeller or similar mechanical agitation equipment, by revolving or shaking the culture vessel (e.g., tube or flask) or by various pumping equipment. Aeration may be further controlled by the passage of sterile air or oxygen through the medium (e.g., through the

fermentation mixture). Also preferably, microorganisms of the present invention are cultured without excess foaming (*e.g.*, *via* addition of antifoaming agents).

Moreover, microorganisms of the present invention can be cultured under controlled temperatures. The term "controlled temperature" includes any temperature which results in production of the desired product (*e.g.*, a B6 vitamer). In one embodiment, controlled temperatures include temperatures between 15°C and 95°C. In another embodiment, controlled temperatures include temperatures between 15°C and 70°C. Preferred temperatures are between 20°C and 55°C, more preferably between 30°C and 50°C.

Microorganisms can be cultured (*e.g.*, maintained and/or grown) in liquid media and preferably are cultured, either continuously or intermittently, by conventional culturing methods such as standing culture, test tube culture, shaking culture (*e.g.*, rotary shaking culture, shake flask culture, etc.), aeration spinner culture, or fermentation. In a preferred embodiment, the microorganisms are cultured in shake flasks. In a more preferred embodiment, the microorganisms are cultured in a fermentor (*e.g.*, a fermentation process). Fermentation processes of the present invention include, but are not limited to, batch, fed-batch and continuous processes or methods of fermentation. The phrase "batch process" or "batch fermentation" refers to a closed system in which the composition of media, nutrients, supplemental additives and the like is set at the beginning of the fermentation and not subject to alteration during the fermentation, however, attempts may be made to control such factors as pH and oxygen concentration to prevent excess media acidification and/or microorganism death. The phrase "fed-batch process" or "fed-batch" fermentation refers to a batch fermentation with the exception that one or more substrates or supplements are added (*e.g.*, added in increments or continuously) as the fermentation progresses. The phrase "continuous process" or "continuous fermentation" refers to a system in which a defined fermentation media is added continuously to a fermentor and an equal amount of used or "conditioned" media is simultaneously removed, preferably for recovery of the desired product (*e.g.*, a B6 vitamer). A variety of such processes have been developed and are well-known in the art.

The phrase "culturing under conditions such that a desired compound is produced" includes maintaining and/or growing microorganisms under conditions (*e.g.*, temperature, pressure, pH, duration, etc.) appropriate or sufficient to obtain production of the desired compound or to obtain desired yields of the particular compound being produced. For example, culturing is continued for a time sufficient to produce the desired amount of a compound (*e.g.*, a B6 vitamer). Preferably, culturing is continued for a time sufficient to substantially reach suitable production of the compound (*e.g.*, a

time sufficient to reach a suitable concentration of a B6 vitamer). In one embodiment, culturing is continued for about 12 to 24 hours. In another embodiment, culturing is continued for about 24 to 36 hours, 36 to 48 hours, 48 to 72 hours, 72 to 96 hours, 96 to 120 hours, 120 to 144 hours, or greater than 144 hours. The methodology of the present invention can further include a step of recovering a desired compound (e.g., a B6 vitamer). The term "recovering" a desired compound includes extracting, harvesting, isolating or purifying the compound from culture media. Recovering the compound can be performed according to any conventional isolation or purification methodology known in the art including, but not limited to, treatment with a conventional resin (e.g., anion or cation exchange resin, non-ionic adsorption resin, etc.), treatment with a conventional adsorbent (e.g., activated charcoal, silicic acid, silica gel, cellulose, alumina, etc.), alteration of pH, solvent extraction (e.g., with a conventional solvent such as an alcohol, ethyl acetate, hexane and the like), dialysis, filtration, concentration, crystallization, recrystallization, pH adjustment, lyophilization and the like. For example, a compound can be recovered from culture media by first removing the microorganisms from the culture. The resulting solutions are then passed through or over a cation exchange resin to remove cations and/or through or over an anion exchange resin to purify or concentrate the desired product. The resulting compound can subsequently be converted to a salt (e.g., a chloride or sulfate salt) by ion exchange.

Preferably, a desired compound of the present invention is "extracted," "isolated" or "purified" such that the resulting preparation is substantially free of other media components (e.g., free of media components and/or fermentation byproducts). The language "substantially free of other media components" includes preparations of the desired compound in which the compound is separated from media components or fermentation byproducts of the culture from which it is produced. In one embodiment, the preparation has greater than about 80% (by dry weight) of the desired compound (e.g., less than about 20% of other media components or fermentation byproducts), more preferably greater than about 90% of the desired compound (e.g., less than about 10% of other media components or fermentation byproducts), still more preferably greater than about 95% of the desired compound (e.g., less than about 5% of other media components or fermentation byproducts), and most preferably greater than about 98-99% desired compound (e.g., less than about 1-2% other media components or fermentation byproducts). When the desired compound has been derivatized to a salt, the compound is preferably further free of chemical contaminants associated with the formation of the salt. When the desired compound has been derivatized to an alcohol, the compound is preferably further free of chemical contaminants associated with the formation of the alcohol.

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In an alternative embodiment, the desired compound is not purified from the microorganism, for example, when the microorganism is biologically non-hazardous (*e.g.*, safe). For example, the entire culture (or culture supernatant) can be used as a source of product (*e.g.*, crude product). In one embodiment, the culture (or culture supernatant) is used without modification. In another embodiment, the culture (or culture supernatant) is concentrated. In yet another embodiment, the culture (or culture supernatant) is dried or lyophilized.

Preferably, a production method of the present invention results in production of the desired compound, *e.g.*, a B6 vitamer, at a significantly high yield. The phrase "significantly high yield" includes a level of production or yield which is sufficiently elevated or above what is usual for comparable production methods, for example, which is elevated to a level sufficient for commercial production of the desired product (*e.g.*, production of the product at a commercially feasible cost). In one embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 5 mg/L. In another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 10 mg/L. In another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 50 mg/L. In yet another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 150 mg/L.

Depending on the biosynthetic enzyme or combination of biosynthetic enzymes manipulated, it may be desirable or necessary to provide (*e.g.*, feed) microorganisms of the present invention at least one biosynthetic precursor such that the desired compound or compounds are produced. The term "biosynthetic precursor" or "precursor" includes an agent or compound which, when provided to, brought into contact with, or included in the culture medium of a microorganism, serves to enhance or increase biosynthesis of the desired product. In one embodiment, the biosynthetic precursor or precursor is glutamine. In another embodiment, the biosynthetic precursor or precursor is ribose. The amount of glutamine or ribose added is preferably an amount that results in a concentration in the culture medium sufficient to enhance productivity of the microorganism (*e.g.*, a concentration sufficient to enhance production of a B6 vitamer). The term "excess ribose or glutamine" includes ribose or glutamine levels increased or higher than those routinely utilized for culturing the microorganism in

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question. For example, culturing the *Bacillus* microorganisms described in the instant Examples is routinely done in the presence of about 0-5 g/L ribose or glutamine.

Accordingly, excess ribose or glutamine levels can include levels of about 5-10 g/L or more preferably about 5-20 g/L ribose or glutamine. Biosynthetic precursors of the

5 present invention can be added in the form of a concentrated solution or suspension (e.g., in a suitable solvent such as water or buffer) or in the form of a solid (e.g., in the form of a powder). Moreover, biosynthetic precursors of the present invention can be added as a single aliquot, continuously or intermittently over a given period of time.

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This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application are incorporated herein by reference.

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EXAMPLES

EXAMPLE 1: Biological assay for B6 vitamers using *Saccharomyces uvarum*.

Quantitation of B6 vitamers in supernatants of cultures of micro-organisms or extracts of organisms that have been genetically modified to increase production of B6 vitamers is conveniently done using *Saccharomyces uvarum* (formerly and still often named *S. carlsbergensis*) strain ATCC 9080 as the indicator strain or test organism. The method is essentially that described in the Difco Manual (1984, Difco Laboratories, Detroit, MI, 10th Edition, pp. 1104-1106), with the modification that 50 mg/liter of streptomycin sulfate is added to the liquid growth medium for the test organism. However, any other appropriate indicator organism may be used, together with a medium that is appropriate for that organism that is free of B6 vitamers. For example, an *E. coli* *padB* mutant can be used in a standard minimal medium that is well known in the art, such as M9 glucose minimal medium (Miller, J., (1972) Experiments in Molecular Genetics, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

When using *S. uvarum* strain ATCC 9080 as the indicator strain, Bacto Pyridoxine Y Medium (Difco Laboratories, available through VWR Scientific, Inc.), supplemented with 50 mg/liter streptomycin sulfate, is used for the serial dilutions, and PN, PL, or PM is used to generate the standard curve. The responses to these three standard compounds are almost identical to each other with *S. uvarum* strain ATCC 9080 (Figure 3).

EXAMPLE 2: Deletion of a portion of the *yaaDE* operon in *B. subtilis*.

The *SOR* and *SNO* genes of *Cercospora nicotianae* were originally identified by mutations that lead to hypersensitivity to singlet oxygen-generating reagents (Ehrenschaft, M., et al. (1999) *Proc. Natl. Acad. Sci. USA* 96: 9347-9378). Mutations in either of these genes also lead to PL auxotrophy. The protein sequences obtained from translation of the *SOR* and *SNO* open reading frames were used as homology probes to search through the *B. subtilis* genome sequence using the BLAST homology search program of the Subtilist website. The *SOR* protein was significantly homologous to the YaaD protein, and the *SNO* protein was significantly homologous to the YaaE protein. Moreover, the genes encoding the YaaD and YaaE proteins (namely *yaaD* and *yaaE*) occur adjacent to each other on the *B. subtilis* chromosome as a two gene operon.

General methods for growth, storage, transformation, and molecular biology of *B. subtilis* strains are given in Harwood, C., and Cutting, S. (1990), *Molecular Biological Methods for Bacillus*, John Wiley and Sons, New York, NY, hereby

incorporated in its entirety by reference. The *yaaDE* operon DNA sequence was amplified using the Polymerase Chain Reaction (PCR) with Pfu Turbo DNA polymerase (Stratagene, Inc., used according to the manufacturer's instructions). The DNA primers used were RY395 (SEQ ID NO:1) and RY396 (SEQ ID NO:2). RY395, the upstream
5 primer, introduces an *XbaI* site and artificial ribosome binding site. RY396, the downstream primer, introduces a *BamHI* site. The template DNA was chromosomal DNA isolated from wild type *B. subtilis* strain PY79. The blunt ended PCR product was ligated into the *EcoRV* site of pGEM5Zf(+) (Promega, Inc.) to give plasmid pAN368. Next, a gram positive chloramphenicol resistance gene on a blunt DNA fragment was
10 ligated into pAN368 that had been cut with *HpaI*, to give plasmid pDX1F (SEQ ID NO:5, Figure 4). pDX1F therefore is deleted for a portion of *yaaD* and a portion of *yaaE*. pDX1F was used to transform wild type *B. subtilis* strain PY79 to 5 mg/liter chloramphenicol resistance, and a double crossover event was confirmed using PCR and the same primers used to clone *yaaDE*. The resulting strain was named PX1.

15 PX1 was able to grow on Spizizen's minimal medium with trace elements (SMM) (Harwood, C., and Cutting, S. (1990) *Molecular Biological Methods for Bacillus*, John Wiley and Sons, New York, NY, pp. 548-549) supplemented with 2 μ M pyridoxal HCl (Sigma-Aldrich Chemical Co.), but it did not grow without the supplement. Thus it was established that at least one of *yaaD* or *yaaE* is required for
20 PLP synthesis in *B. subtilis*.

EXAMPLE 3: Deletion of *yhaF* in *B. subtilis*.

The protein sequence of the *E. coli pdxF* gene was used as a probe to search the *B. subtilis* genome as described in Example 1. The only significant homolog
25 was *yhaF*. In a fashion similar to that of Example 1, the *yhaF* was cloned and deleted from the chromosome of PY79 using plasmid pDX11F (SEQ ID NO:6, Figure 5), to give strain PX11. The PCR primers used to clone *yhaF* were RY407 (SEQ ID NO:3) and RY408 (SEQ ID NO:4). The restriction sites used for insertion of the antibiotic resistance gene were the *PshAI* and *EheI* sites in the *yhaF* coding region. PX11 is a
30 serine auxotroph, but not a PL auxotroph. By comparison to *E. coli*, it appears that *yhaF* functions in serine synthesis and probably encodes the equivalent of *SerC*, but that the YhaF protein is not required for PLP synthesis in *B. subtilis*. Therefore, it is established that sequence homology does not necessarily imply functional homology.

35 **EXAMPLE 4: Overexpression of the *yaaDE* operon in *B. subtilis*.**

The *XbaI* to *BamHI* fragment from pAN368 that contains the *yaaDE* operon and artificial ribosome binding site was inserted into either of two expression

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vectors, to yield plasmids pDX14R (SEQ ID NO:7) and pDX17R (SEQ ID NO:8), respectively. In pDX14R and pDX17R, the *yaaDE* operon is expressed from the strong constitutive *B. subtilis* phage SP01 promoters, P_{26} and P_{15} , respectively (see Figures 6 and 7).

5 pDX14R and pDX17R were each transformed into wild type *B. subtilis* strain PY79, selecting for chloramphenicol resistance. The plasmids integrate into the chromosome at the *yaaDE* locus by single crossover. The resulting strains were named PX14 and PX17, respectively.

10 PX14 and PX17 were grown for 48 hours at 37°C in 5 ml test tube cultures in a roller drum at about 100 rotations per minute. The culture medium was SVY (20 g Difco Veal Infusion Broth, 5 g Difco Yeast Extract, 2 g ammonium sulfate, 5 g sodium glutamate, and 30 g glucose per liter, buffered with 200 mM potassium phosphate, pH 7.0). Cells were removed by centrifugation followed by sterile filtration (Millipore 0.45 micron), and the supernatant solutions were assayed for PL equivalents using the biological assay described in Example 1. The parent strain, PY79 was grown and processed in similar fashion as a control. The uncultured SVY medium was assayed as another control, since it was likely that the SVY medium contained a measurable level of B6 vitamers. The results are shown in Table 2, below.

20 **Table 2: Production of B6 vitamers by *Bacillus subtilis* derivatives in 48 hour test tube cultures grown in SVY**

Strain	Cassette	Integration Target	OD ₆₀₀	Total B6 Vitamers ¹ mg/liter	Net B6 Vitamers ² mg/liter
PX14	$P_{26}yaaDE$	<i>yaaDE</i>	17	7.2	7.0
PX17	$P_{15}yaaDE$	<i>yaaDE</i>	17	4.9	4.7
PX1	$\Delta yaaDE$	<i>yaaDE</i>	8	0.4	0.2
PY79	-	-	19	0.8	0.6
(Medium)	-	-	0.08	0.2	(0)

¹ Sum of PN, PL, PM, and derivatives thereof that can be utilized by pyridoxine indicator strain *S. carlbergensis* as a source of vitamin B6 for growth.

25 ² Calculated by subtracting the amount assayed in the medium.

After subtracting the B6 vitamers contained in the medium, strain PX14 produced 7.0 mg/liter PL equivalents, while the parent PY79 produced only 0.6 mg/liter of PL equivalents. Thus, expression of the *yaaDE* operon has been shown to be rate limiting for B6 vitamer production in *B. subtilis*. Moreover, a genetically modified

30

strain, where this rate limiting step was enhanced, produced more than a ten-fold increase in B6 vitamers secretion compared to that of the parent.

EXAMPLE 5: Complementation of *E. coli* *pdx* mutants by plasmids that express the *B. subtilis* *yaaDE* operon.

5 Plasmid pDX14R, described above in Example 4, was used to transform various *E. coli* strains that contained mutations that lacked function in each of the known genes involved in PLP biosynthesis (except for *dxs*, which is an essential gene for *E. coli*). The selection was for resistance to 250 mg/liter ampicillin. Each transformant
10 was then tested for growth on minimal medium (SMM with 0.5 % glucose, see Example 2) supplemented with 100 mg/liter serine, and compared to growth of its respective untransformed parent on the same medium. All mutations tested were complemented by pDX14R. Specifically, *pdxA*, *pdxB*, *pdxF*, *pdxJ*, and *pdxH*, were all complemented by pDX14R. Therefore, expression of the *B. subtilis* *yaaDE* operon in *E. coli* is sufficient
15 for PLP biosynthesis, even in the absence of any one of the above functional *pdx* genes. Several important and unexpected conclusions or inferences can be drawn from these results. First, the substrate(s) for the enzyme(s) encoded by *yaaDE* must be present in *E. coli*, even when a biosynthetic intermediate normally used to make PLP is absent or greatly reduced. Second, PNP or PLP is possibly the product of the enzyme(s) encoded
20 by *yaaDE*. Third, since an early block in the *E. coli* PLP biosynthetic pathway (for example that in a *pdxB* mutant) does not prevent *yaaDE* from complementation, the substrates for the enzyme(s) encoded by *yaaDE* are not likely to be the same as for the last step in PNP or PLP synthesis in wild type *E. coli*. These unexpected results lead to the possibility of producing B6 vitamers using *B. subtilis* *yaaDE* or the homologous
25 genes from another organism (for example, but not limited to, *SOR* and *SNO* from *Cercospora nicotianae* or *PDX1* and *PDX2* from *S. cerevisiae*) in a heterologous host species, including, but not limited to, *E. coli* and *Oryza sativa*.

EXAMPLE 6: Overexpression of the *yaaDE* operon in *E. coli*.

30 Plasmids pDX14R and pDX17R were transformed into *E. coli* strain DH5 α (New England Biolabs), selecting for ampicillin resistance. The transformants were grown for 48 hours in 5 ml test tube cultures at 37°C, and the supernatants were worked up as in Example 3. The assay results for PL equivalents are shown in Table 3, below.
35

Table 3: Production of B6 vitamers by *Escherichia coli* harboring plasmids containing engineered *Bacillus subtilis* genes¹

Strain	Plasmid Cassette	OD ₆₀₀	Total B6 Vitamers ² mg/liter	Net B6 Vitamers ³ mg/liter
DH5α	<i>P₂₆yaaDE</i>	7.6	3.2	3.1
DH5α	<i>P₁₅yaaDE</i>	8.2	3.2	3.1
DH5α	-	9	0.1	(0)

¹ *E. coli* test tube cultures are grown in SVY for 48 hours.² Sum of PN, PL, PM, and derivatives thereof that can be utilized by pyridoxine indicator strain *S. carlbergensis* as a source of vitamin B6 for growth.³ Calculated by subtracting the amount assayed in DH5α not containing plasmid.

Thus it has been shown that the *yaaD* and *yaaE* genes can be expressed in a heterologous host strain, and B6 vitamers can still be overproduced. By extension of this approach, the *yaaD* and *yaaE* genes of *B. subtilis* can be overexpressed in any organism where an overexpression system exists, and in the resulting strains, B6 vitamers will be overproduced. Overproduction of the rate limiting enzyme for B6 vitamer production in any organism that is capable of producing B6 vitamers will lead to overproduction of B6 vitamers.

The YaaD and YaaE protein sequences were used as probes to search the NCBI database for homologs in plants using the BLAST™ program which can be found at the National Center for Biotechnology Information website (Altschul S.F (1990) *J. Mol. Biol.* 215(3):403-10). Several homologs of YaaD were found in several genera of plants, including *Arabidopsis*, *Oryza*, *Ginkgo*, *Hevea*, *Phaseolus*, and *Stellaria*. Two homologs of YaaE were found in *Arabidopsis thaliana*. However, no homologs of *pdxA* and *pdxJ* were found. Therefore the plant kingdom appears to use the Type B Pathway for B6 vitamer biosynthesis. Thus for example, overexpression of the YaaD homolog (GenBank accession number AAL73561) from *Oryza sativa* (rice), and the *A. thaliana* homolog of YaaE (GenBank accession number AB011483) together in a plant using methods well known in the art, such as expression from the Cauliflower Mosaic Virus 35S promoter, will lead to overproduction of B6 vitamers in that plant.

EXAMPLE 7: Other routes to increasing the activity of enzymes involved in B6 vitamer synthesis.

The overexpression of the *yaaDE* operon leads to an increase in the amount of the encoded enzyme(s), which in turn leads to an increase in the total activity of said enzyme(s). Increase in this activity leads to an increase in the production B6 vitamer. Other methods can be used to increase the activity of the relevant enzyme(s)

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under conditions of B6 vitamer production. For example, in addition to increasing the amount of a relevant enzyme(s), the total activity of the relevant enzyme(s) can be increased by mutating the gene(s) to increase the specific activity of the enzyme(s), and/or by mutating the gene(s) to encode a feedback resistant variant of the enzyme(s).

- 5 Such desirable mutations can be obtained by screening large numbers of mutants for the increased activity as evidenced by an increase in B6 vitamer production as described in Example 4, or by selecting for mutants that are resistant to inhibitors that are specific for the PLP biosynthetic pathway, and screening among those mutants for an increase in B6 vitamer production. Examples of such inhibitors are isoniazid, iproniazid, and
- 10 ginkgotoxin (4'-methoxy pyridoxine) (Dempsey and Arcement (1971) J. Bacteriol. 107(2): 580-582; Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570; Fiehe, K., et al., (2000) J. Nat. Prod. 63(2): 185-189).

15 **EXAMPLE 8: Processing of biosynthetic B6 vitamers.**

- A B6 vitamer produced by a genetically modified organism of the invention can be harvested and processed into a format that is appropriate for commercial use. For example, after culturing a B6 vitamer producing micro-organism in liquid culture, the entire culture, including cells can be dried by evaporation or by spray
- 20 drying, and the resulting powder can be mixed into animal feeds. Alternatively, the cells can be first removed by centrifugation or filtration, and the resulting supernatant solution can be dried as described above. As another alternative, the B6 vitamer can be purified from the culture broth by techniques well known in the art, such as filtration, reverse osmosis, column chromatography (ion exchange, hydrophobic or hydrophilic
- 25 adsorption, gel filtration, etc.), solvent extraction, precipitation, distillation, evaporation, and the like. If the B6 vitamer producing organism is a plant, then the appropriate portion of the plant (for example the leaves, stems, roots, flowers, fruits, seeds, or any combination thereof) can be harvested and processed. For example the plant material can be dried and used directly, or the material can be pulverized or ground and the B6
- 30 vitamer extracted and/or processed as described above for cultures.

The production organism can be a micro-organism that normally inhabits the gut of humans or an animal of interest (for example one of many bacteria of the genus *Lactobacillus*, such as *L. acidophilus*), and the B6 vitamer can be delivered by ingestion of the organism.

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Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

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What is claimed:

1. An organism that has been genetically modified to comprise a recombinant DNA molecule that results in the increase of the activity of one or more enzymes that catalyze(s) a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism.
2. The organism of claim 1, wherein B6 vitamer production is at least ten-fold higher than from the unmodified parent organism.
3. The organism of claim 1, wherein said enzyme is one or more of YaaD or YaaE.
4. The organism of claim 1, wherein said organism is genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer.
5. The organism of claim 4, wherein said genes are derived from *Bacillus*.
6. The organism of claim 4, wherein said genes are derived from *Bacillus subtilis*.
7. The organism of claim 4, wherein at least one of said genes is a *yaaD* gene.
8. The organism of claim 4, wherein at least one of said genes is a *yaaE* gene.
9. The organism of claim 4, wherein at least two of said genes are *yaaD* and *yaaE* genes.
10. The organism of claim 4, wherein said organism is a *Bacillus* strain.

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11. The organism of claim 4, wherein said organism is *Bacillus subtilis*.
12. The organism of any one of claims 1-11, wherein said organism is grown in a liquid culture and the total B6 vitamer concentration in the culture supernatant is at least 7.0 mg/liter.
13. A method of producing a B6 vitamer comprising culturing a microorganism that has been genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism, under conditions such that the B6 vitamer is produced.
14. The method of claim 13, wherein said enzyme is one or more of YaaD or YaaE.
15. The method of claim 13, wherein at least one of said genes is a *yaaD* gene.
16. The method of claim 13, wherein at least one of said genes is a *yaaE* gene.
17. The method of claim 13, wherein said genes are contained on the *yaaDE* operon.
18. The method of claim 13, wherein the B6 vitamer is pyridoxine.
19. The method of claim 13, wherein the B6 vitamer is pyridoxal.
20. The method of claim 13, wherein the B6 vitamer is pyridoxamine.
21. The method of claim 13, wherein the said genes are bacterial-derived.
22. The method of claim 13, wherein said genes are derived from *Bacillus*.

23. The method of claim 13, wherein said genes are derived from *Bacillus subtilis*.
- 5 24. The method of claim 13, wherein the microorganism is Gram positive.
25. The method of claim 13, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*,
10 *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.
26. The method of claim 13, wherein the microorganism is of the genus *Bacillus*.
- 15 27. The method of claim 13, wherein the microorganism is *Bacillus subtilis*.
28. The method of claim 13, further comprising recovering the B6 vitamer.
20
29. A method of producing a B6 vitamer comprising culturing a microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene under conditions such that the B6 vitamer is produced.
- 25 30. The method of claim 29, wherein the microorganism overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic enzyme.
31. The method of claim 29, wherein the B6 vitamer is pyridoxine.
- 30 32. The method of claim 29, wherein the B6 vitamer is pyridoxal.
33. The method of claim 29, wherein the B6 vitamer is pyridoxamine.
34. The method of claim 29, wherein the microorganism
35 overexpresses at least two B6 vitamer biosynthetic enzymes.

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35. The method of claim 29, wherein the microorganism is Gram positive.
36. The method of claim 29, wherein the microorganism is Gram negative.
37. The method of claim 29, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.
38. The method of claim 29, wherein the microorganism is of the genus *Bacillus*.
39. The method of claim 29, wherein the microorganism is *Bacillus subtilis*.
40. The method of claim 29, further comprising recovering the B6 vitamer.
41. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene.
42. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic enzyme.
43. The method of claim 42, wherein said enzyme is YaaD or YaaE.
44. The recombinant microorganism of claim 41 that overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.
45. The recombinant microorganism of claim 41, wherein the B6 vitamer biosynthetic gene is selected from the group consisting of *yaaD* and *yaaE*.
46. The recombinant microorganism of claim 41, that is Gram positive.

47. The recombinant microorganism of claim 41 belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.
- 5 48. The recombinant microorganism of claim 41 belonging to the genus *Bacillus*.
49. The recombinant microorganism of claim 41 which is *Bacillus subtilis*.
- 10 50. A recombinant microorganism selected from the group consisting of PX14 and PX17.
51. A vector comprising a nucleic acid sequence that encodes at least
15 one *Bacillus* B6 vitamer biosynthetic gene operably linked to regulatory sequences.
52. The vector of claim 51, comprising a nucleic acid sequence that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.
- 20 53. The vector of claim 51, wherein the regulatory sequences comprise a constitutively active promoter.
54. The vector of claim 51, wherein the constitutively active promoter comprises P_{15} (SEQ ID NO:9) or P_{26} (SEQ ID NO:10) sequences.
- 25 55. The vector of claim 51, wherein the regulatory sequences comprise at least one artificial ribosome binding site (RBS).
56. A vector selected from the group consisting of pDX14R and
30 pDX17R.
57. A recombinant microorganism comprising the vector of claim 56.
58. An isolated nucleic acid molecule that encodes at least one
35 *Bacillus* B6 vitamer biosynthetic gene.

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59. The isolated nucleic acid molecule of claim 58 that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

60. An isolated *Bacillus* B6 vitamer biosynthetic enzyme polypeptide.

61. An isolated *Bacillus subtilis* B6 vitamer biosynthetic enzyme polypeptide.

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**METHODS AND ORGANISMS FOR
PRODUCTION OF B6 VITAMERS**

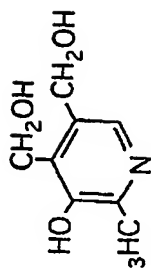
5 Abstract of the Disclosure

The present invention features methods of producing B6 vitamers that involve culturing an organism overexpressing an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer under conditions such that a B6 vitamer is produced. The

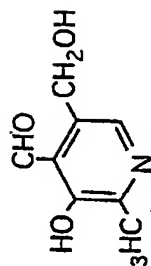
- 10 present invention further features methods of producing B6 vitamers that involve culturing recombinant microorganisms that overexpress at least one B6 vitamer biosynthetic gene, *e.g.*, *yaaD* or *yaaE*.

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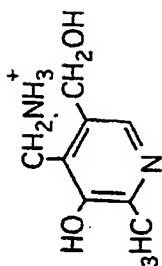
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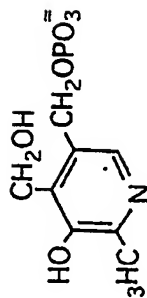
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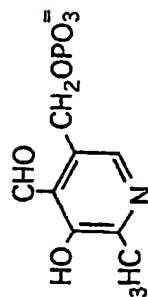
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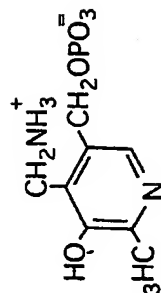
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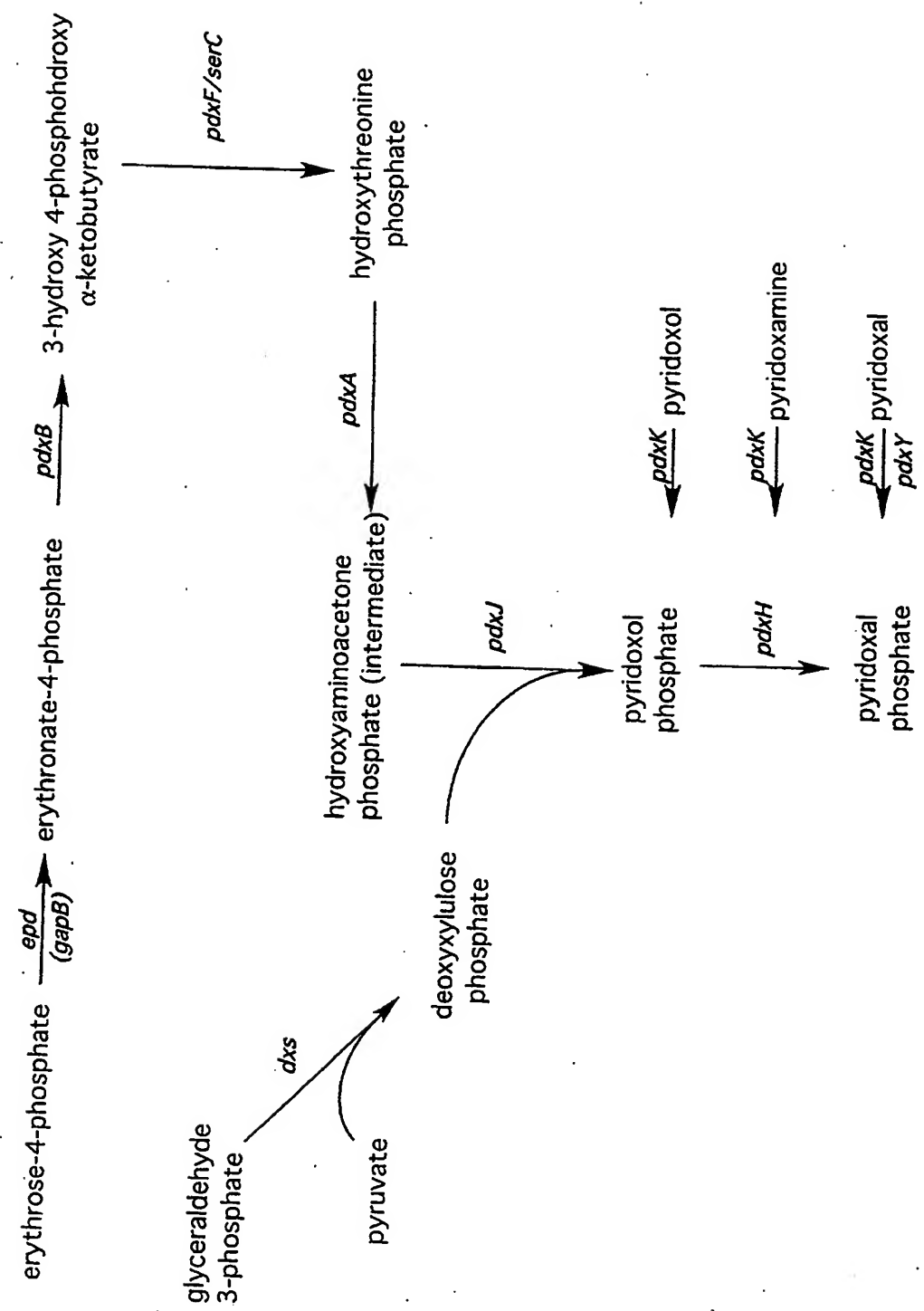
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Figure 2



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Figure 3

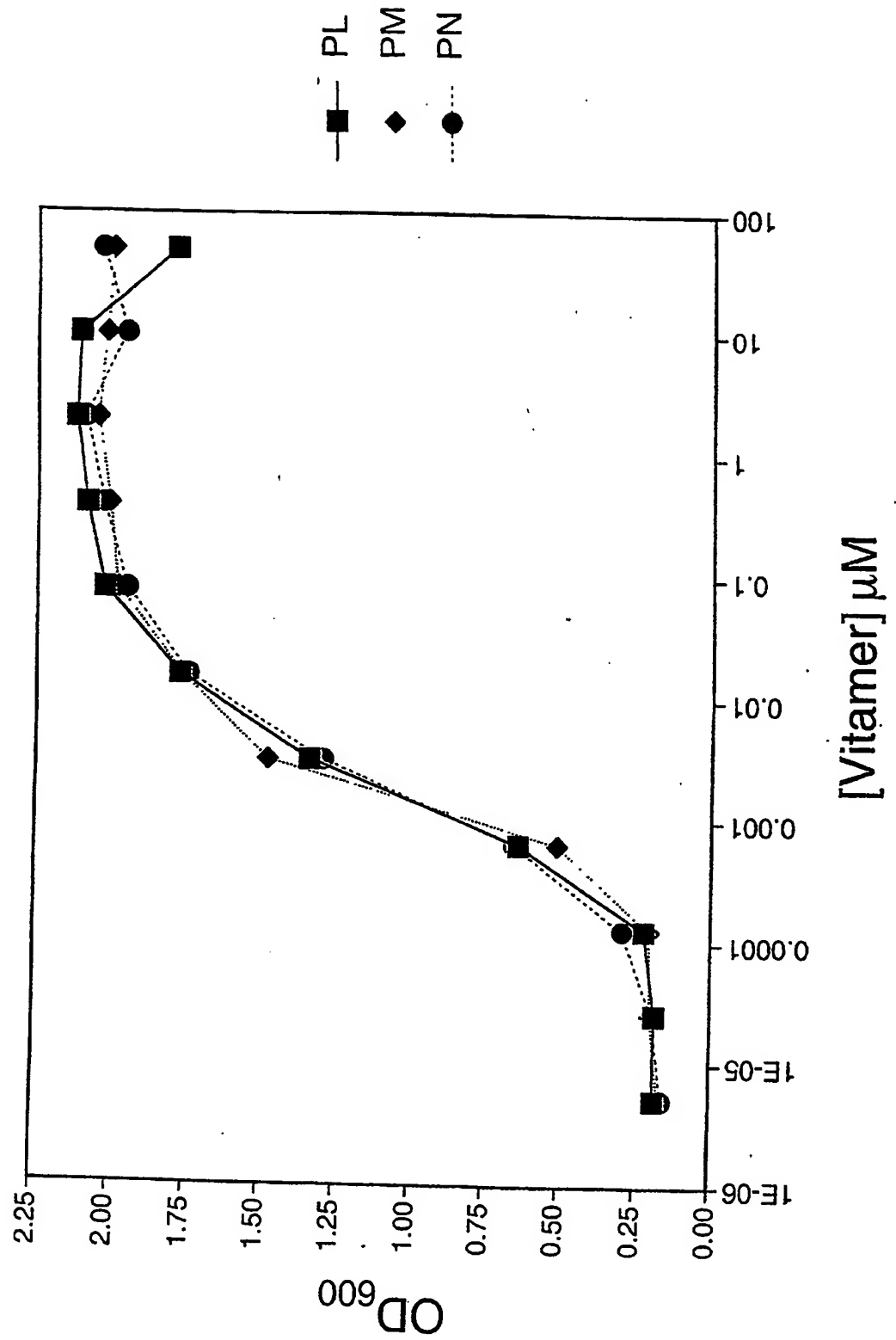


Figure 4. Structure of pDX1F

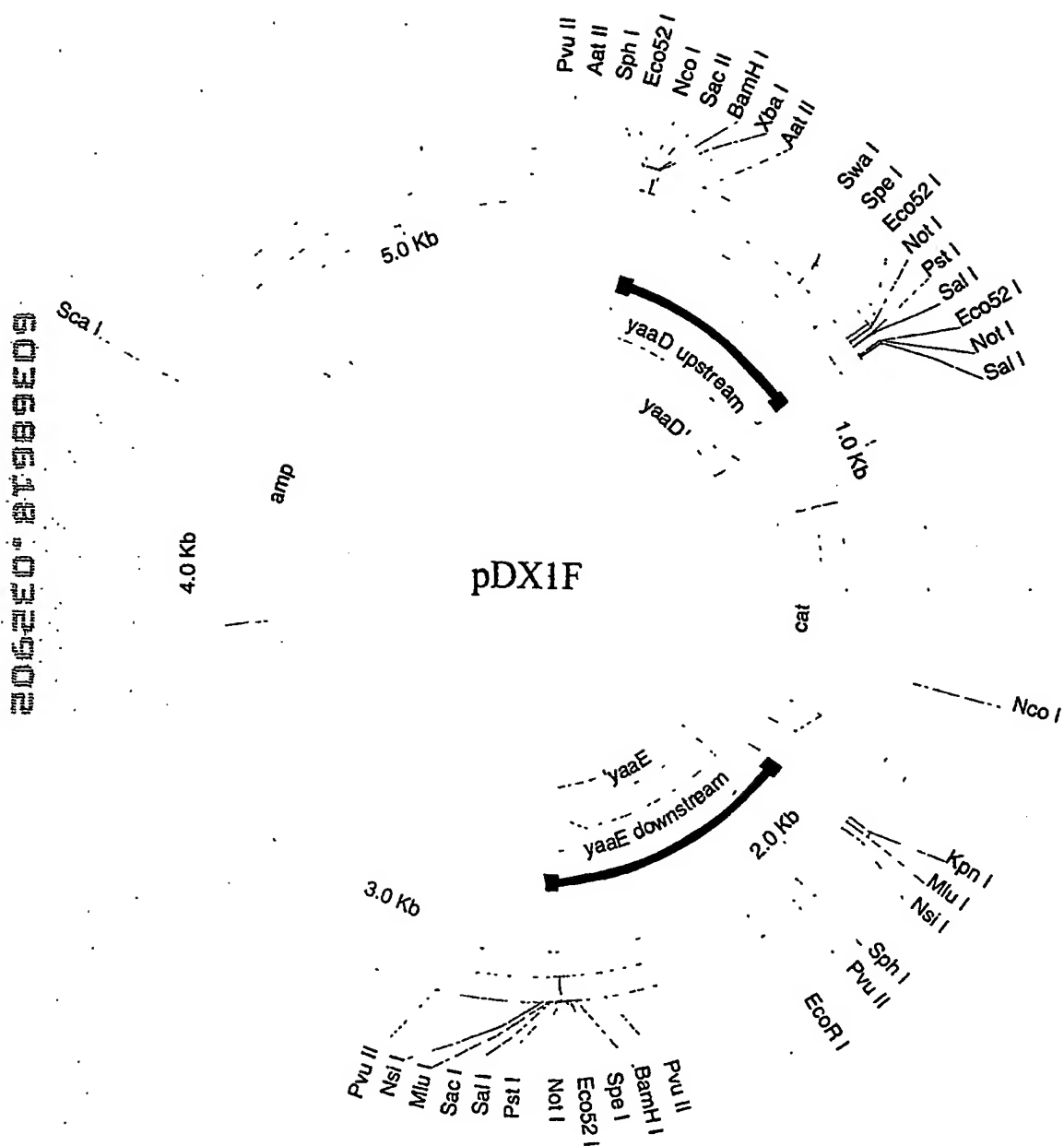


Figure 5. Structure of pDX11F

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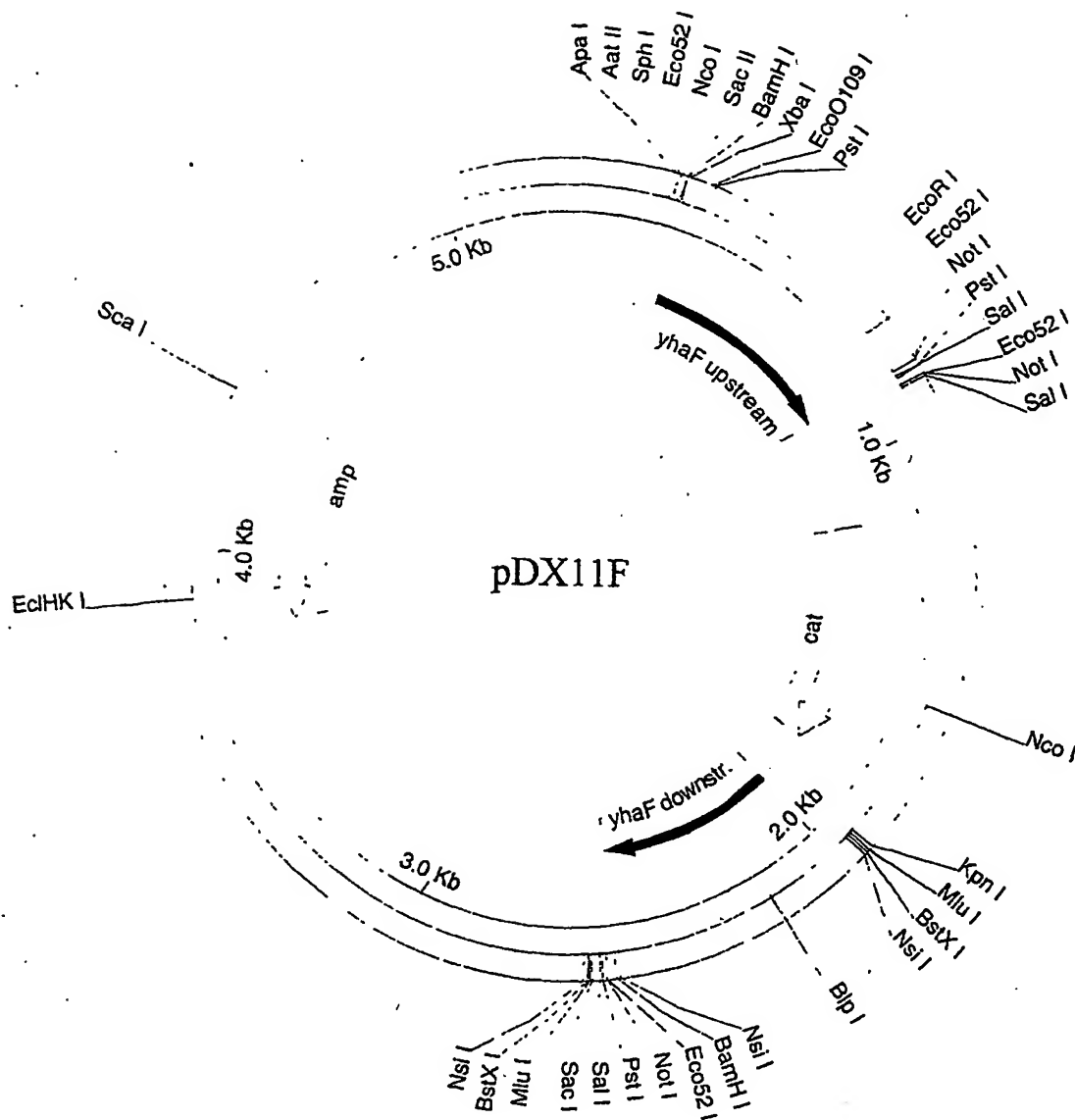
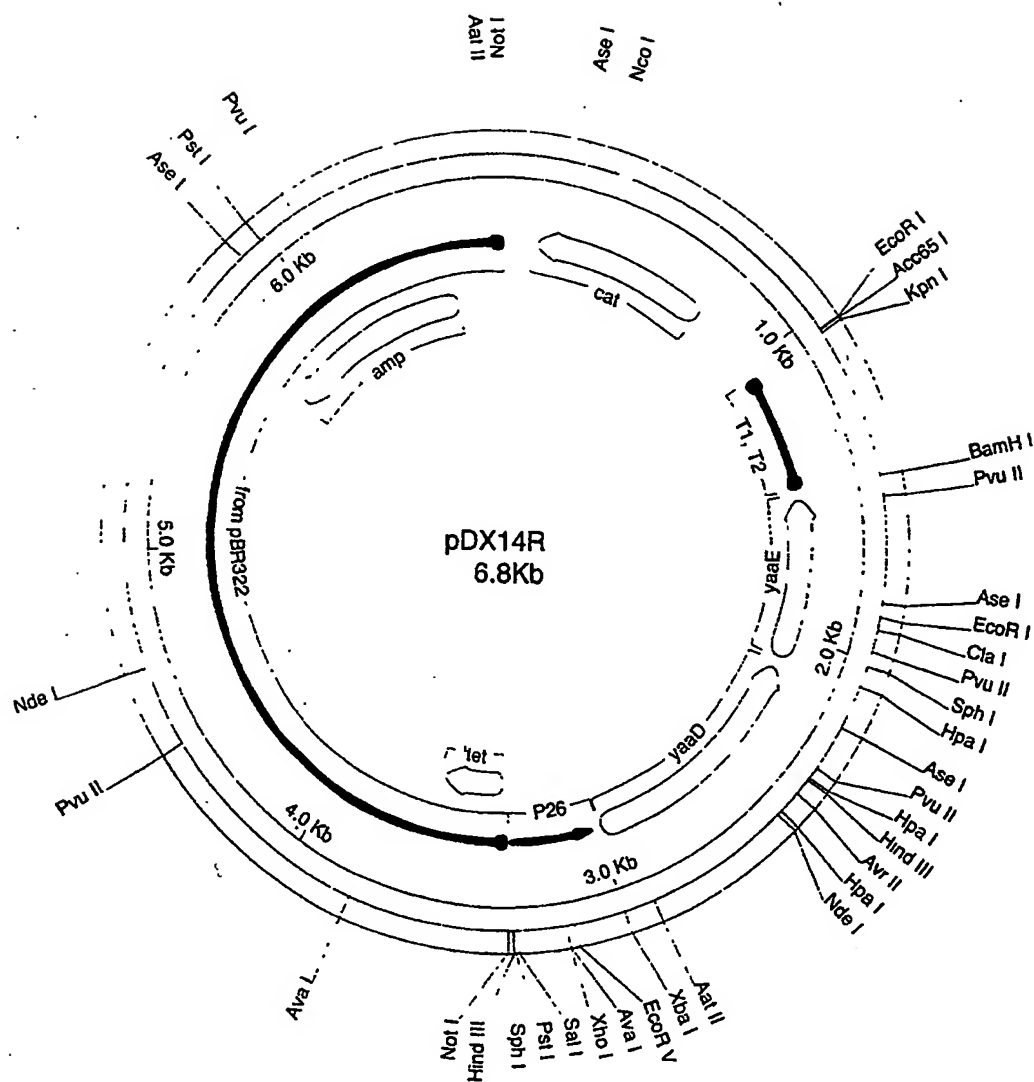
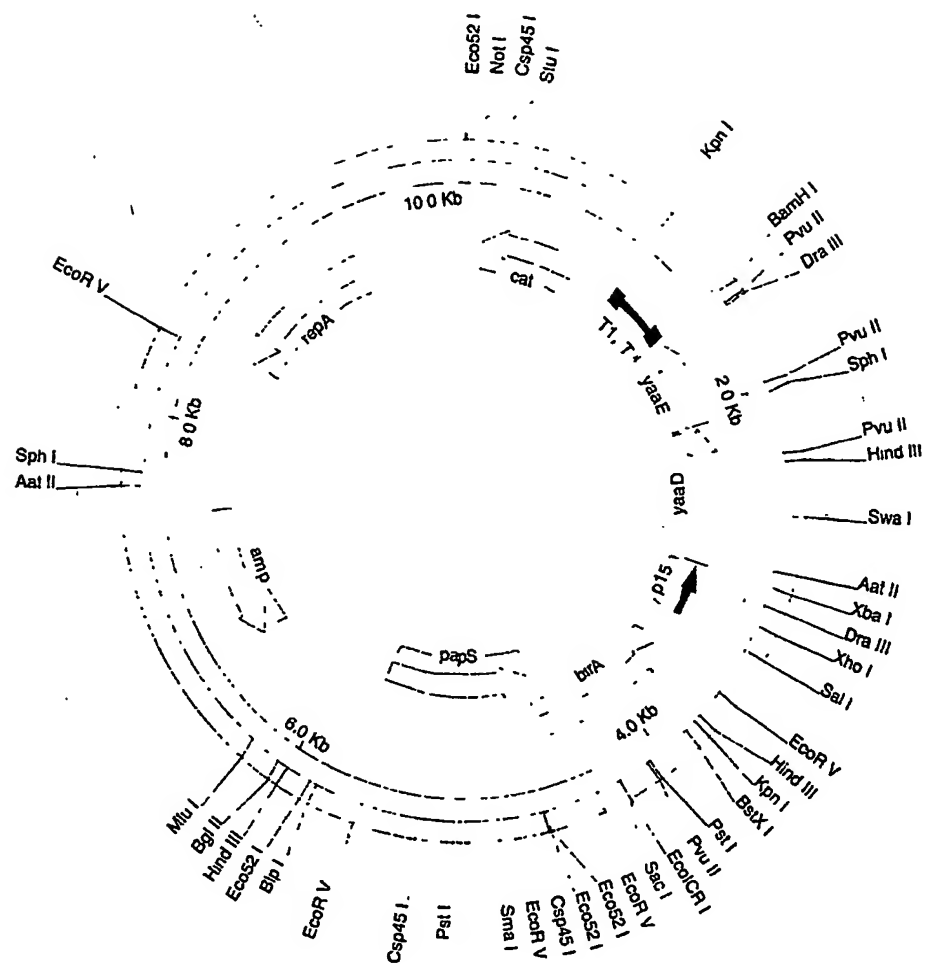


Figure 6



GOVERNMENT OF THE DISTRICT OF COLUMBIA



SEQUENCE LISTING

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<223> ribosome binding site

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27

20625018.032901

EMBL-EBI

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EMBOSS Transeq

Transeq translates nucleic acid sequences to the corresponding peptide sequence. It can translate 3 forward or three reverse sense frames, or in all three forward or reverse frames, or in all six frames.

Frame

1 ☐

Regions

START-END

Table

Standard Code

Trim

No ☐

Reverse

No ☐

Col

No ☐

Enter or Paste a nucleic acid Sequence in any format:

```

atggctgaat tactgttagg cgtcaacatt gaccatatcg ctacgctgcg caacgcg
ggtaccgctt acccgatcc ggtgcaggcc gcgtttattg ccgagcaggc gggagcg
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ctgcgtcaga cgctggatac ccgcatgaat ctggagatgg cggtgaccga agagatg
gcgatcgccg ttgagacgaa gccacatttt tgctgcctgg taccggaaaa gcgtcag
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gatgccaaaa ctgacgccga acaggcgcaa gagctggcgc gtatcgccaa agccgcg
tttgccgcaa gcctcgggtc gaaagttaac gccggacacg gtctgaccta tcacaac

```

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EMBOSS Transeq Results


Transeq Results	
Frame	1
Translation table	Standard (0)
Regions	START-END
Trim	no
Reverse	no
Color	no
Transeq output	transeq-20090202-16070285811681.output
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FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE
ARG*
```

BLAST Basic Local Alignment Search Tool

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Protein Sequence (243 letters)

Results for: lcl|79748 None(243aa) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|79748

Description

None

Molecule type

amino acid

Query Length

243

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#) [\[Related Structures\]](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hittlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Feb 1, 2009 5:55 PM
Number of letters	2,685,767,600
Number of sequences	7,788,834

Entrez query none

Karlin-Altschul statistics

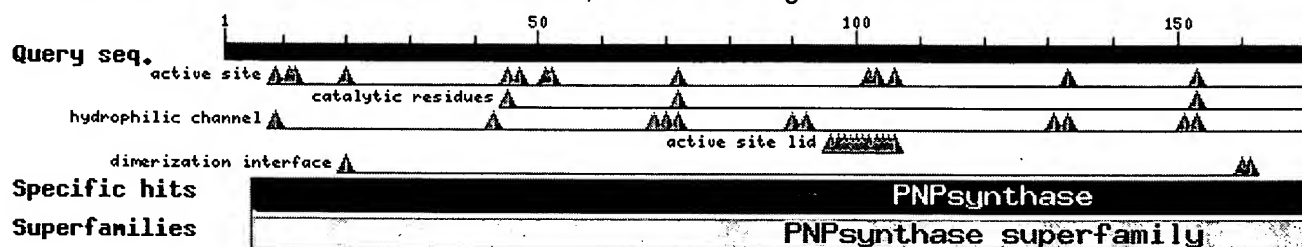
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K	0.133588	0.041
H	0.375908	0.14

Results Statistics

Length adjustment	131
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Effective search space	186528198752
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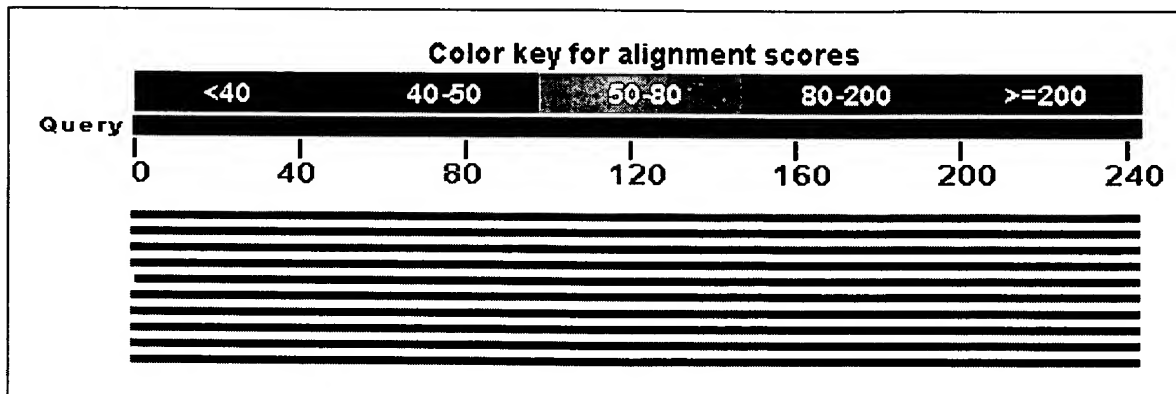
Graphic SummaryShow Conserved Domains

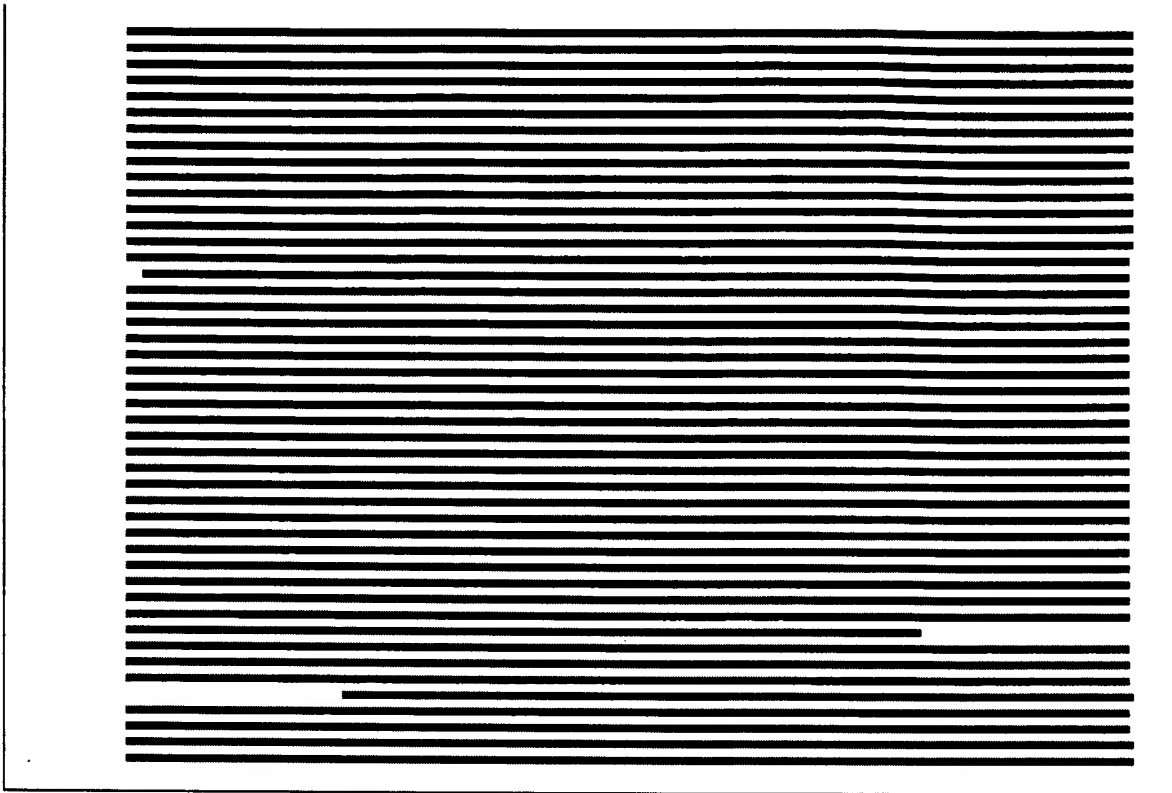
Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 100 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

		Score	
E		(Bits)	Value
Sequences producing significant alignments:			
ref NP_311457.1	pyridoxal phosphate biosynthetic protein Pdx...	491	3e-137
ref YP_002330339.1	pyridoxine 5'-phosphate synthase [Escheri...	489	6e-137
ref NP_289121.1	pyridoxal phosphate biosynthetic protein Pdx...	489	1e-136
ref YP_404339.1	pyridoxal phosphate biosynthetic protein Pdx...	488	1e-136
pdb 1HQ1 A	Chain A, Crystal Structure Of Pyridoxine 5'-Phosph...	488	1e-136
ref YP_001744753.1	pyridoxine 5'-phosphate synthase [Escheri...	488	2e-136
ref YP_403963.1	pyridoxal phosphate biosynthetic protein Pdx...	486	6e-136
ref NP_838137.1	pyridoxal phosphate biosynthetic protein Pdx...	486	6e-136
ref YP_311545.1	pyridoxal phosphate biosynthetic protein Pdx...	486	9e-136
ref ZP_02902009.1	pyridoxine 5'-phosphate synthase [Escheric...	485	1e-135
ref YP_541876.1	pyridoxal phosphate biosynthetic protein Pdx...	484	3e-135
gb ABK20147.1	pyridoxal phosphate biosynthetic protein [Shig...	483	4e-135
ref YP_670456.1	pyridoxal phosphate biosynthetic protein Pdx...	483	5e-135
ref NP_754969.1	pyridoxal phosphate biosynthetic protein Pdx...	482	1e-134
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ref YP_001451819.1	pyridoxal phosphate biosynthetic protein ...	480	5e-134
ref YP_001336529.1	pyridoxal phosphate biosynthetic protein ...	462	1e-128
ref YP_002237093.1	pyridoxine 5'-phosphate synthase [Klebsie...	462	1e-128
ref ZP_03283638.1	hypothetical protein ENTCAN_03445 [Enterob...	461	2e-128
ref NP_457107.1	pyridoxal phosphate biosynthetic protein Pdx...	461	3e-128
ref NP_461513.1	pyridoxal phosphate biosynthetic protein Pdx...	460	4e-128
ref YP_149621.1	pyridoxal phosphate biosynthetic protein Pdx...	460	4e-128
ref YP_001569382.1	pyridoxal phosphate biosynthetic protein ...	459	1e-127
ref YP_002147536.1	pyridoxine 5'-phosphate synthase [Salmone...	458	2e-127
ref YP_001177766.1	pyridoxal phosphate biosynthetic protein ...	451	3e-125
ref ZP_03086581.1	pyridoxal phosphate biosynthetic protein P...	451	3e-125
ref YP_001436809.1	pyridoxal phosphate biosynthetic protein ...	437	3e-121
ref ZP_00822617.1	COG0854: Pyridoxal phosphate biosynthesis ...	397	4e-109
ref ZP_00830259.1	COG0854: Pyridoxal phosphate biosynthesis ...	394	3e-108
ref YP_001005353.1	pyridoxal phosphate biosynthetic protein ...	393	5e-108
ref YP_001400120.1	pyridoxal phosphate biosynthetic protein ...	392	2e-107
ref NP_663623.1	pyridoxal phosphate biosynthetic protein Pdx...	391	2e-107
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ref ZP_00833834.1	COG0854: Pyridoxal phosphate biosynthesis ...	390	4e-107
ref ZP_00827187.1	COG0854: Pyridoxal phosphate biosynthesis ...	390	4e-107
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ref YP_051364.1	pyridoxal phosphate biosynthetic protein Pdx...	390	7e-107
ref YP_001479390.1	pyridoxal phosphate biosynthetic protein ...	382	1e-104
ref YP_455464.1	pyridoxal phosphate biosynthetic protein Pdx...	381	3e-104
ref NP_930557.1	pyridoxal phosphate biosynthetic protein Pdx...	376	7e-103
ref YP_855346.1	pyridoxal phosphate biosynthetic protein Pdx...	376	9e-103
ref ZP_03318787.1	hypothetical protein PROVALCAL_01725 [Prov...	373	7e-102
ref ZP_02961267.1	hypothetical protein PROSTU_03281 [Provide...	373	7e-102
ref YP_002151612.1	pyridoxal phosphate biosynthetic protein ...	372	1e-101
ref YP_001143199.1	pyridoxal phosphate biosynthetic protein ...	372	2e-101
ref ZP_03315319.1	hypothetical protein PROVRUST_02121 [Provi...	367	4e-100

ref ZP_01262022.1	pyridoxal phosphate biosynthetic protein [...]	361	3e-98
ref ZP_03385196.1	pyridoxal phosphate biosynthetic protein P...	360	4e-98
ref YP_205467.1	pyridoxal phosphate biosynthetic protein Pdx...	360	5e-98
ref YP_002073491.1	pyridoxal phosphate biosynthetic protein ...	358	1e-97
ref YP_002156883.1	pyridoxal phosphate biosynthetic protein ...	358	2e-97
ref ZP_03400922.1	pyridoxal phosphate biosynthetic protein P...	357	5e-97
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ref ZP_01816562.1	pyridoxal phosphate biosynthetic protein P...	354	3e-96
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ref ZP_01161526.1	pyridoxal phosphate biosynthetic protein [...]	353	7e-96
ref YP_002127690.1	pyridoxal phosphate biosynthetic protein ...	353	1e-95
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ref YP_588729.1	pyridoxal phosphate biosynthetic protein Pdx...	352	1e-95
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ref YP_734973.1	pyridoxal phosphate biosynthetic protein Pdx...	335	3e-90
ref YP_339261.1	pyridoxal phosphate biosynthetic protein Pdx...	334	4e-90
ref YP_002359017.1	pyridoxal phosphate biosynthetic protein ...	334	4e-90
ref YP_001365462.1	pyridoxal phosphate biosynthetic protein ...	334	4e-90
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ref YP_751604.1	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
ref YP_964373.1	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
ref YP_001673314.1	pyridoxal phosphate biosynthetic protein ...	330	7e-89
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ref YP_001759633.1	pyridoxal phosphate biosynthetic protein ...	329	1e-88
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ref NP_716971.1	pyridoxal phosphate biosynthetic protein Pdx...	328	2e-88
ref YP_942095.1	pyridoxal phosphate biosynthetic protein Pdx...	326	3e-88

ref|YP_693348.1| pyridoxal phosphate biosynthetic protein Pdx... 328 3e-88

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>ref|NP_311457.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c
O157:H7 str. Sakai]

ref|NP_417059.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12
substr. MG1655]

ref|AP_003150.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12
substr. W3110]

71 more sequence titles

ref|YP_001463887.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia
E24377A]

ref|YP_001459361.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichi
HS]

ref|ZP_02773388.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4113]

ref|ZP_02782782.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4401]

ref|ZP_02786192.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4501]

ref|ZP_02793675.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4486]

ref|ZP_02798517.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4196]

ref|ZP_02803548.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4076]

ref|ZP_02812931.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC869]

ref|ZP_02823953.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC508]

ref|YP_001724107.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichi
ATCC 8739]

ref|YP_001731493.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K
DH10B]

ref|ZP_03002699.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c
53638]

ref|ZP_03029794.1| pyridoxine 5'-phosphate synthase [Escherichia coli B7A]

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ref|ZP_03049293.1| pyridoxine 5'-phosphate synthase [Escherichia coli E110019]

ref|ZP_03061820.1| pyridoxine 5'-phosphate synthase [Escherichia coli B171]

ref|ZP_03069709.1| pyridoxine 5'-phosphate synthase [Escherichia coli 101-1]

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O157:H7 str. EC4024]

ref|ZP_03251256.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4206]

ref|ZP_03255815.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4045]

ref|ZP_03259661.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4042]

ref|YP_002272039.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O157:H
EC4115]

ref|YP_002294127.1| **G** pyridoxal phosphate biosynthetic protein [Escherichia col

ref|ZP_03442750.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
TW14588]

ref|YP_002381699.1| **G** pyridoxine 5'-phosphate synthase [Escherichia fergusonii
35469]

ref|YP_002388058.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli IAI1]

ref|YP_002403859.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli 55989]

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sp|P0A795.2|PDXJ_ECO57 RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

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Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate

pdb|1M5W|B **S** Chain B, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate
Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate

pdb|1M5W|C **S** Chain C, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
 pdb|1M5W|D **S** Chain D, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
 pdb|1M5W|E **S** Chain E, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
 pdb|1M5W|F **S** Chain F, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
 pdb|1M5W|G **S** Chain G, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
 pdb|1M5W|H **S** Chain H, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
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 gb|AAA21845.1| pdxJ
 gb|AAA79826.1| CG Site No. 416
 gb|AAC75617.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12 substr. MG1655]
 dbj|BAB36853.1| **G** pyridoxine biosynthesis [Escherichia coli O157:H7 str. Sakai]
 dbj|BAE76740.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K12 sub W3110]
 gb|ABV06978.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli HS]
 gb|ABV20635.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli E24377A]
 gb|ACA76780.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli ATCC 8739]
 gb|ACB03715.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K12 su DH10B]
 gb|EDU34578.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4196]
 gb|EDU55194.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4113]
 gb|EDU65731.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 53638]
 gb|EDU72247.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4076]
 gb|EDU73719.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4401]
 gb|EDU80638.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4486]
 gb|EDU86799.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4501]
 gb|EDU90661.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC869]
 gb|EDU97102.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC508]
 gb|EDV61746.1| pyridoxine 5'-phosphate synthase [Escherichia coli B7A]
 gb|EDV82886.1| pyridoxine 5'-phosphate synthase [Escherichia coli E22]
 gb|EDV88722.1| pyridoxine 5'-phosphate synthase [Escherichia coli E110019]
 gb|EDX28996.1| pyridoxine 5'-phosphate synthase [Escherichia coli B171]
 gb|EDX39410.1| pyridoxine 5'-phosphate synthase [Escherichia coli 101-1]
 gb|EDZ78321.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4206]
 gb|EDZ84450.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4045]
 gb|EDZ87146.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4042]
 gb|ACI35060.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str EC4115]
 dbj|BAG78376.1| **G** pyridoxal phosphate biosynthetic protein [Escherichia coli SE
 gb|EEC27459.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. TW14588]
 emb|CAU98723.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 emb|CAQ88058.1| **G** pyridoxine 5'-phosphate synthase [Escherichia fergusonii]
 emb|CAQ99513.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 Length=243

GENE ID: 914900 ECs3430 | pyridoxal phosphate biosynthetic protein PdxJ
 [Escherichia coli O157:H7 str. Sakai] (Over 10 PubMed links)

Score = 491 bits (1263), Expect = 3e-137, Method: Compositional matrix adjust.
Identities = 243/243 (100%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG 243
Sbjct 241  ARG 243

```

>ref|YP_002330339.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O127:H E2348/69]

ref|YP_002413587.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli UMN026
emb|CAS10389.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O127:H6 st E2348/69]

emb|CAR14061.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
Length=243

GENE ID: 7062394 **pdxJ** | pyridoxine 5'-phosphate synthase
[Escherichia coli O127:H6 E2348/69] (10 or fewer PubMed links)

Score = 489 bits (1260), Expect = 6e-137, Method: Compositional matrix adjust.
Identities = 242/243 (99%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  KRLA+AGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG 243
Sbjct 241  ARG 243

```

>ref|NP_289121.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c O157:H7_EDL933]

pir||C85902 pyridoxine biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

gb|AAG57679.1|AE005487_3 **G** pyridoxine biosynthesis [Escherichia coli O157:H7 ED Length=243

GENE ID: 957924 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
[Escherichia coli O157:H7 EDL933] (10 or fewer PubMed links)

Score = 489 bits (1258), Expect = 1e-136, Method: Compositional matrix adjust.
Identities = 242/243 (99%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

```

```

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
Sbjct 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241 ARG 243
Sbjct 241 ARG 243

```

>ref|YP_404339.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella dysenteriae Sd197]

sp|Q32CV7.1|PDXJ SHIDS **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=gb|ABB62848.1| **G** pyridoxine biosynthesis [Shigella dysenteriae Sd197]
Length=243

GENE ID: 3795506 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Shigella dysenteriae Sd197] (10 or fewer PubMed links)

Score = 488 bits (1257), Expect = 1e-136, Method: Compositional matrix adjust.
Identities = 242/243 (99%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
Sbjct 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241 ARG 243
Sbjct 241 ARG 243

```

>pdb|1H01|A **S** Chain A, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase

pdb|1H01|B **S** Chain B, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase

pdb|1H01|C **S** Chain C, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
21 more sequence titles

pdb|1H01|D **S** Chain D, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase

pdb|1H04|A **S** Chain A, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1H04|B **S** Chain B, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1H04|C **S** Chain C, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1H04|D **S** Chain D, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1IXN|A **S** Chain A, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXN|B **S** Chain B, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXN|C **S** Chain C, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

Synthase

pdb|1IXN|D **S** Chain D, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|A **S** Chain A, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|B **S** Chain B, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|C **S** Chain C, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|D **S** Chain D, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|A **S** Chain A, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|B **S** Chain B, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|C **S** Chain C, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|D **S** Chain D, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|A **S** Chain A, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|B **S** Chain B, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|C **S** Chain C, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|D **S** Chain D, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
 Length=242

Score = 488 bits (1257), Expect = 1e-136, Method: Compositional matrix adjust.
 Identities = 242/242 (100%), Positives = 242/242 (100%), Gaps = 0/242 (0%)

Query	2	AELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	61
		AELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Sbjct	1	AELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	62	RQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQREVTEGGLDVAGQDQKMRDACK	121
		RQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQREVTEGGLDVAGQDQKMRDACK	
Sbjct	61	RQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQREVTEGGLDVAGQDQKMRDACK	120
Query	122	RLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATF	181
		RLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATF	
Sbjct	121	RLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATF	180
Query	182	AASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLEA	241
		AASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLEA	
Sbjct	181	AASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLEA	240
Query	242	RG	243
		RG	
Sbjct	241	RG	242

>ref|YP_001744753.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli SMS-3-
 ref|YP_002408707.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli IAI39]
 gb|ACB18311.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli SMS-3-5]
 emb|CAR18891.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 Length=243

GENE ID: 6143419 **pdxJ** | pyridoxine 5'-phosphate synthase
 [Escherichia coli SMS-3-5]

Score = 488 bits (1256), Expect = 2e-136, Method: Compositional matrix adjust.
 Identities = 241/243 (99%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

Query	1	MAELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		MAELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Sbjct	1	MAELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60

```

Query   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC   120
Sbjct   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ+KMRDAC   120

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT   180
Sbjct   121  KRLA+AGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT   180

Query   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240

Query   241   ARG   243
Sbjct   241   ARG   243

```

>ref|YP_408963.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella boyd Sb227]
 ref|YP_001881343.1| **G** pyridoxine 5'-phosphate synthase [Shigella boydii CDC 308 sp|Q31XS3.1|PDXJ SHIBS RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN gb|ABB67135.1| **G** pyridoxine biosynthesis [Shigella boydii Sb227]
 gb|ACD10043.1| **G** pyridoxine 5'-phosphate synthase [Shigella boydii CDC 3083-94] Length=243

GENE ID: 3781575 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Shigella boydii Sb227] (10 or fewer PubMed links)

Score = 486 bits (1252), Expect = 6e-136, Method: Compositional matrix adjust.
 Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

```

Query   1   MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60
Sbjct   1   MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60

Query   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC   120
Sbjct   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ+KMRDAC   120

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT   180
Sbjct   121  KRLDAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELRIAKAAT   180

Query   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240

Query   241   ARG   243
Sbjct   241   ARG   243

```

>ref|NP_838137.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 2a str. 2457T]
 ref|NP_708416.2| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 2a str. 301]
 ref|YP_690029.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 5 str. 8401]
 ref|ZP_03064347.1| pyridoxine 5'-phosphate synthase [Shigella dysenteriae 1012]
 gb|AAP17947.1| **G** pyridoxal phosphate biosynthetic protein [Shigella flexneri 2a str. 2457T]
 gb|AAN44123.2| **G** pyridoxal phosphate biosynthetic protein [Shigella flexneri 2a str. 301]
 gb|ABF04724.1| **G** pyridoxine biosynthesis [Shigella flexneri 5 str. 8401]
 gb|EDX35667.1| pyridoxine 5'-phosphate synthase [Shigella dysenteriae 1012] Length=243

GENE ID: 1079066 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Shigella flexneri 2a str. 2457T] (10 or fewer PubMed links)

Score = 486 bits (1251), Expect = 6e-136, Method: Compositional matrix adjust.
 Identities = 240/243 (98%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQOR+K+RDAC 120
LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQREKIRDAC 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQEL RIAKAAT 180
KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELVRIAKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG 243
Sbjct 241  ARG 243

```

>ref|YP_311545.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella sonnei Ss046]
 sp|Q3YYV2.1|PDXJ SHISS **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
 gb|AA289310.1| **G** pyridoxine biosynthesis [Shigella sonnei Ss046]
 Length=243

GENE ID: 3669253 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
 [Shigella sonnei Ss046] (10 or fewer PubMed links)

Score = 486 bits (1250), Expect = 9e-136, Method: Compositional matrix adjust.
 Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQOR+KMRDAC 120
LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQREKMRDAC 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  KRLDAGIQ+SLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQEL RIAKAAT 180
KRLTDAGIQISLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELVRIAKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG 243
Sbjct 241  ARG 243

```

>ref|ZP_02902009.1| pyridoxine 5'-phosphate synthase [Escherichia albertii TW076
 gb|EDS92821.1| pyridoxine 5'-phosphate synthase [Escherichia albertii TW07627]
 Length=243

Score = 485 bits (1249), Expect = 1e-135, Method: Compositional matrix adjust.
 Identities = 240/243 (98%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQOR KMRDAC 120
LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRGKMRDAC 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  KRLADAGIQVSLFIDADEEQIKAAA+VGAPFIEIHTGCIYADAKTDAEQAQELARIAKAA+ 180
KRLADAGIQVSLFIDADEEQIKAAAADVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAS 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

```

Query 241 ARG 243
Sbjct 241 ARG 243

>ref|YP_541876.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89]

ref|YP_853698.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli APEC 01]

gb|ABE08345.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89]

gb|ABJ01984.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli APEC 01]
Length=248

GENE ID: 3989796 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89] (10 or fewer PubMed links)

Score = 484 bits (1245), Expect = 3e-135, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDV I	
Sbjct	6	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVCI	65
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
		LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	
Sbjct	66	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQREKMRDAC	125
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	180
		KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	
Sbjct	126	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	185
Query	181	FAASLGLKVNAGHGLTYHNKAIATAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		FAASLGLKVNAGHGLTYHNKAIATAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	
Sbjct	186	FATSLSGLKVNAGHGLTYHNKAIATAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	245
Query	241	ARG	243
		ARG	
Sbjct	246	ARG	248

>gb|ABK20147.1| pyridoxal phosphate biosynthetic protein [Shigella boydii]
Length=243

Score = 483 bits (1244), Expect = 4e-135, Method: Compositional matrix adjust.
Identities = 238/243 (97%), Positives = 239/243 (98%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADG TVHLREDRRRHITDRDVRI	
Sbjct	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGTTVHLREDRRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
		LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	
Sbjct	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQREKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	180
		KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	
Sbjct	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELVRIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNKAIATAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		FAASLGLKVNAGHGLTYHNKAIATAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	
Sbjct	181	FAASLGLKVNAGHGLTYHNKAIATAIPEMHELNIGHAIIGRAVMTGLKDTVAEMKRLMLE	240
Query	241	ARG	243
		ARG	
Sbjct	241	ARG	243

>ref|YP_670456.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536]

ref|ZP_03035524.1| pyridoxine 5'-phosphate synthase [Escherichia coli F11]

ref|YP_002392398.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli S88]
7 more sequence titles

ref|YP_002398892.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli ED1a]
 ref|YP_002557403.1| **G** Pyridoxine 5'-phosphate synthase [Escherichia coli LF82]
 gb|ABG70555.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536]
 gb|EDV65320.1| pyridoxine 5'-phosphate synthase [Escherichia coli F11]
 emb|CAR04001.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 emb|CAR09161.2| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 emb|CAP77010.1| **G** Pyridoxine 5'-phosphate synthase [Escherichia coli LF82]
 Length=243

GENE ID: 4190772 ECP 2566 | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536] (10 or fewer PubMed links)

Score = 483 bits (1244), Expect = 5e-135, Method: Compositional matrix adjust.
 Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVEMKRLMLE	240
Sbjct	181	FATSLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>ref|NP_754969.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli CFT073]

gb|AAN81537.1|AE016764_219 **G** Pyridoxal phosphate biosynthetic protein pdxJ [Esc CFT073]
 Length=248

GENE ID: 1038793 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli CFT073] (10 or fewer PubMed links)

Score = 482 bits (1241), Expect = 1e-134, Method: Compositional matrix adjust.
 Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	6	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVI	65
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	66	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	125
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	126	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	185
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVEMKRLMLE	240
Sbjct	186	FATSLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVEMKRLMLE	245
Query	241	ARG 243	
Sbjct	246	ARG 248	

>sp|Q8FF18.3|PDXJ_ECOL6 RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 Length=243

Score = 482 bits (1240), Expect = 1e-134, Method: Compositional matrix adjust.
Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

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Query 1  MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDV I 60


Query 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
Sbjct 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120


Query 121 KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 KRLADAGIQVSLFIDADE+QIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 FA SLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241 ARG 243
Sbjct 241 ARG 243

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>ref|YP_001451819.1|  pyridoxal phosphate biosynthetic protein PdxJ [Citrobacte ATCC BAA-895]

gb|ABV11383.1|  hypothetical protein CK0_00218 [Citrobacter koseri ATCC BAA-89 Length=243]

GENE ID: 5585068 CKO 00218 | pyridoxal phosphate biosynthetic protein PdxJ [Citrobacter koseri ATCC BAA-895]

Score = 480 bits (1235), Expect = 5e-134, Method: Compositional matrix adjust.
Identities = 236/243 (97%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

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Query 1  MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60


Query 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
Sbjct 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120


Query 121 KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 KRLADAGI VSLFIDADEEQIKAAA+VGAP+IEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 FAASLGLKVNAGHGLTYHNV+AI AA+PEMHELNIGHAIIGRAVM+GLK+AVAEMKRLMLE 240

Query 241 ARG 243
Sbjct 241 ARG 243

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>ref|YP_001336529.1|  pyridoxal phosphate biosynthetic protein PdxJ [Klebsiella subsp. pneumoniae MGH 78578]

gb|ABR78299.1|  pyridoxal phosphate biosynthetic protein [Klebsiella pneumonia subsp. pneumoniae MGH 78578]
Length=243

GENE ID: 5342763 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]

Score = 462 bits (1188), Expect = 1e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 236/243 (97%), Gaps = 0/243 (0%)

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Query 1  MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
Sbjct 61  LRQTL TRMNLEMAVTEEML IA ET KPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

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Sbjct 121 +RLADAGI VSLFIDADE QIKAAA+VGAP+IEIHTGCIYADAKTDAEQQA+EL RIAKAAT
          QRLADAGILVSLFIDADEAQIKAAAADVGAPYIEIHTGCIYADAKTDAEQARELERIAKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVM+GLK+AVAEMK LMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAIAAALPEMHELNIGHAIIGRAVMSGLKEAVAEMKRLMLE 240
Query 241 ARG 243
          ARG
Sbjct 241 ARG 243

```

>ref|YP_002237093.1| **G** pyridoxine 5'-phosphate synthase [Klebsiella pneumoniae 3
gb|ACI11352.1| G pyridoxine 5'-phosphate synthase [Klebsiella pneumoniae 342]
Length=243

GENE ID: 6934996 **pdxJ** | pyridoxine 5'-phosphate synthase
[Klebsiella pneumoniae 342] (10 or fewer PubMed links)

Score = 462 bits (1188), Expect = 1e-128, Method: Compositional matrix adjust.
Identities = 227/243 (93%), Positives = 236/243 (97%), Gaps = 0/243 (0%)

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Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
          LR+TL TRMNLEMAVTEEML IA ETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC
Sbjct 61 LRETLDTRMNLEMAVTEEMLTACETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAA+VGAPFIEIHTGCIYADAKTDAEQQAQELARIAKAAT 180
          +RLADAGI VSLFIDAD EQIKAAA+VGAP+IEIHTGCIYADAKTDA QA+EL RIAKAAT
Sbjct 121 QRLADAGILVSLFIDADNEQIKAAAADVGAPYIEIHTGCIYADAKTDAGQAKELERIAKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVM+GLK+AVAEMKRLMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAIAAALPEMHELNIGHAIIGRAVMSGLKEAVAEMKRLMLE 240
Query 241 ARG 243
          ARG
Sbjct 241 ARG 243

```

>ref|ZP_03283638.1| hypothetical protein ENTCAN_03445 [Enterobacter cancerogenus
ATCC 35316]
gb|EEA13217.1| hypothetical protein ENTCAN_03445 [Enterobacter cancerogenus
ATCC 35316]
Length=243

Score = 461 bits (1187), Expect = 2e-128, Method: Compositional matrix adjust.
Identities = 227/242 (93%), Positives = 235/242 (97%), Gaps = 0/242 (0%)

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Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
          LRQTLDTMRNLEMAVTEEMLAIA ETKPHFCCLVPEKRQEVTTTEGGLDVAGQ +KMRDAC
Sbjct 61 LRQTLDTMRNLEMAVTEEMLAIAACETKPHFCCLVPEKRQEVTTTEGGLDVAGQPEKMRDAC 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAA+VGAPFIEIHTGCIYADAKTDAEQQAQELARIAKAAT 180
          KRLADAGI VSLFIDAD+ QIKAAA+ GAP+IEIHTGCIYADAK DAEQA+EL RIAKAAT
Sbjct 121 KRLADAGILVSLFIDADDAQIKAAAADAGAPYIEIHTGCIYADAKNDAEQAKELERIAKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVM+GLKDAVAEMKRLMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAIAAALPEMHELNIGHAIIGRAVMSGLKDAVAEMKRLMLE 240
Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|NP_457107.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en
subsp. enterica serovar Typhi str. CT18]

ref|NP_804155.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en
subsp. enterica serovar Typhi str. Ty2]

ref|ZP_03358029.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. E02-1180]


7 more sequence titles


ref|ZP_03364950.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. E98-0664]

ref|ZP_03370878.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. E98-2068]

ref|ZP_03376409.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. J185]

sp|Q8Z4K6.2|PDXJ_SALTI RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
pir||AH0828 probable pyridoxal phosphate biosynthetic protein STY2824 [imported - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)]


emb|CAD02780.1|  putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Typhi]

gb|AA068004.1|  putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Typhi Ty2]
Length=243

GENE ID: 1249133 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Salmonella enterica subsp. enterica serovar Typhi str. CT18]
(10 or fewer PubMed links)

Score = 461 bits (1185), Expect = 3e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	MAELLLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Query	61	LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTLHTRM NLEMAVTEEM LAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGCYA+A+TDAEQA+ELARIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	AA LGLKVNAGHGLTYHNVKAI AA+PEMHELNIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>ref|NP_461513.1|  pyridoxal phosphate biosynthetic protein PdxJ [Salmonella typhimurium str. LT2]

ref|ZP_02343149.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]


ref|ZP_02573805.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]


26 more sequence titles


ref|ZP_02663381.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]

ref|ZP_02668300.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]


ref|ZP_02683344.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]

ref|YP_002041841.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL254]

ref|YP_002046640.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]

ref|YP_002115641.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

ref|ZP_03165472.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]

ref|YP_002216645.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]

ref|ZP_03220482.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Javiana str. GA MM04042433]

ref|YP_002227475.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella subsp. enterica serovar Gallinarum str. 287/91]

ref|YP_002244636.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella subsp. enterica serovar Enteritidis str. P125109]

sp|Q8ZN19.2|PDXJ SALTY RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

gb|AAL21472.1| **G** carries out condensation and ring closure step after PdxA in pyridoxine biosynthesis [Salmonella typhimurium LT2]

gb|ACF64860.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL254]

gb|ACF66310.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]

gb|ACF91091.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

gb|EDY26273.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]

gb|EDY28219.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]

gb|ACH75352.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Dublin str. CT 02021853]

gb|EDZ06327.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433]

emb|CAR38432.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella ent subsp. enterica serovar Gallinarum str. 287/91]

gb|EDZ13051.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]

gb|EDZ15860.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]

gb|EDZ24330.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]

gb|EDZ36146.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]

emb|CAR34140.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella ent subsp. enterica serovar Enteritidis str. P125109]

Length=243

GENE ID: 1254100 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella typhimurium LT2] (10 or fewer PubMed links)

Score = 460 bits (1184), Expect = 4e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	MAELLLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Query	61	LRQTL DTRM NLEM AVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRD KMRDAC	120
Sbjct	61	LRQTL TRM NLEM AVTEEMLAI AVET+PHFCCLVPEKRQEVTTTEGGLDVAGQRD KMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGCIYA+A+TDAEQA+ELARIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHelnIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	AA LGLKVNAGHGLTYHNVKAIAA+PEMHEL NIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Query	241	ARG	243
Sbjct	241	ARG	243

>ref|YP_149621.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Paratyphi A str. ATCC 9150]

ref|YP_217560.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Choleraesuis str. SC-B67]

ref|YP_001586617.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella subsp. enterica serovar Paratyphi B str. SPB7]

17 more sequence titles

ref|ZP_02657214.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp.

enterica serovar Kentucky str. CDC 191]
 ref|ZP_02700515.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
 ref|ZP_02833432.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537]
 ref|ZP_03075503.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
 ref|YP_002141117.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
 ref|ZP_03214396.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]
 sp|Q57LD3.1|PDXJ_SALCH RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 sp|Q3V7K1.1|PDXJ_SALPA RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 gb|AAV76309.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
 gb|AAX66479.1| **G** carries out condensation and ring closure step after PdxA in pyridoxine biosynthesis [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
 gb|ABX65784.1| **G** hypothetical protein SPAB_00348 [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]
 gb|EDX44722.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
 gb|EDX49461.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
 emb|CAR58387.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
 gb|EDZ03427.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]
 gb|EDZ20478.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191]
 gb|EDZ28717.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537]
 Length=243

GENE ID: 3178757 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] (10 or fewer PubMed links)

Score = 460 bits (1184), Expect = 4e-128, Method: Compositional matrix adjust.
 Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC	120
Sbjct	61	LRQTLHTRM NLEMAVTEEM LAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAAKAT	180
Sbjct	121	RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGCIYA+A+TDAEQA+ELARIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	AA LGLKVNAGHGLTYHNVKAI AA+PEMHENLIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>ref|YP_001569382.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella subsp. arizonae serovar 62:z4,z23:--]

gb|ABX20240.1| **G** hypothetical protein SARI_00300 [Salmonella enterica subsp. ar serovar 62:z4,z23:--]
 Length=243

GENE ID: 5764319 **SARI_00300** | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. arizonae serovar 62:z4,z23:--]

Score = 459 bits (1180), Expect = 1e-127, Method: Compositional matrix adjust.
 Identities = 225/243 (92%), Positives = 233/243 (95%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
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Sbjct 1 MAELL LGVNIDHIATLRNARGT YDPVQAAAFIAEQAGADGITVHLREDRRHI+DRDVRI 60
MAELL LGVNIDHIATLRNARGTDYDPVQAAAFIAEQAGADGITVHLREDRRHISDRDVRI

Query 61 LRQTL DTRMNLEMVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
LRQTL TRMNLEMVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC

Sbjct 61 LRQTLHTRMNLEMVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
RLA AGIQVSLFIDADE QI AA AEVGAFFIEIHTGCIY+AKTDAEQ++ELARIA AAT

Sbjct 121 SRLAAAGIQVSLFIDADEAQINAAAEVGAFFIEIHTGCIYANAKTDAEQSKELARIASAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
A LGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVM+GLK+AVAEMKRLMLE

Sbjct 181 LAVRLGLKVNAGHGLTYHNVKAI AALPEMHELNIGHAIIGRAVMSGLKEAVAEMKRLMLE 240

Query 241 ARG 243
ARG
Sbjct 241 ARG 243

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>ref|YP_002147536.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica sub enterica serovar Agona str. SL483]

gb|ACH50628.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Agona str. SL483]
Length=243

GENE ID: 6793014 pdxJ | pyridoxine 5'-phosphate synthase
[Salmonella enterica subsp. enterica serovar Agona str. SL483]

Score = 458 bits (1179), Expect = 2e-127, Method: Compositional matrix adjust.
Identities = 227/243 (93%), Positives = 233/243 (95%), Gaps = 0/243 (0%)

```

Query 1 MAELL LGVNIDHIATLRNARGTAYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
MAELL LGVNIDHIATLRNARGT YDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI

Sbjct 1 MAELL LGVNIDHIATLRNARGTDYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
LRQTL TRMNLEMVTE MLIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC

Sbjct 61 LRQTLHTRMNLEMVTEAMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
RLA AGIQVSLFIDADE QI AA AEVGAFFIEIHTGCIY+A+TDAEQ+ELARIA AAT

Sbjct 121 ARLAAAGIQVSLFIDADERQINAAAEVGAFFIEIHTGCIYANAETDAEQAKELARIASAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
AA LGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVMTGLK+AVAEMKRLMLE

Sbjct 181 LAARLGLKVNAGHGLTYHNVKAI AALPEMHELNIGHAIIGRAVMTGLKEAVAEMKRLMLE 240

Query 241 ARG 243
ARG
Sbjct 241 ARG 243

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>ref|YP_001177766.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobact 638]

gb|ABP61715.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobacter sp 638]
Length=243

GENE ID: 5111760 Ent638_3051 | pyridoxal phosphate biosynthetic protein PdxJ
[Enterobacter sp. 638]

Score = 451 bits (1160), Expect = 3e-125, Method: Compositional matrix adjust.
Identities = 222/242 (91%), Positives = 233/242 (96%), Gaps = 0/242 (0%)

```

Query 1 MAELL LGVNIDHIATLRNARGTAYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
MAELL LGVNIDHIATLRNARGTAYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDV+I

Sbjct 1 MAELL LGVNIDHIATLRNARGTAYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVKI 60

Query 61 LRQTL DTRMNLEMVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
LRQTL DTRMNLEMVTEEMLAIA ETKPHFCCLVPEKRQEVTTTEGGLDVAGQ+DKMRDAC

Sbjct 61 LRQTL DTRMNLEMVTEEMLAIA CETKPHFCCLVPEKRQEVTTTEGGLDVAGQQDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
KRLADAGI VSLFIDAD +QIKAAA VGAP+IEIHTGCIYADA+ + QA+ELARIAKAAT

Sbjct 121 KRLADAGILVSLFIDADFDQIKAAA AVGAPYIEIHTGCIYADAEDAQAQELARIAKAAT 180

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Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAIA IPEM ELNIGHAIIGRAVM+GLK+AV+EMKRLMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAIAQIPEMFELNIGHAIIGRAVMSGLKEAVSEMKRLMLE 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_03086581.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c
O157:H7-str. EC4024]
Length=239

Score = 451 bits (1159), Expect = 3e-125, Method: Compositional matrix adjust.
Identities = 220/238 (92%), Positives = 230/238 (96%), Gaps = 0/238 (0%)

```

Query 5 LLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILRQT 64
        +LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILRQT
Sbjct 1 MLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILRQT 60

Query 65 LDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDACKRLA 124
        LDTRMNLEMAVTEEMLAIA +TKPHFCCLVPEKRQEVTTTEGGLDVAGQ DKMRDACKRLA
Sbjct 61 LDTRMNLEMAVTEEMLTIACTKPHFCCLVPEKRQEVTTTEGGLDVAGQLDKMRDACKRLA 120

Query 125 DAGIQVSLFIDADEEQIKAAA+EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATFAAS 184
        DAGI VSLFIDAD QIKAAA+VGAP+IEIHTGCIYADAK DAEQA+EL RIAKAAT+AAS
Sbjct 121 DAGILVSLFIDADFAQIKAAA+DVGAPYIEIHTGCIYADAKNDAEQAKELERIAKAATYAAS 180

Query 185 LGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEAR 242
        LGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVM+GLK+AV+EMKRLMLEAR
Sbjct 181 LGLKVNAGHGLTYHNVKAIAALPEMHELNIGHAIIGRAVMSGLKEAVSEMKRLMLEAR 238

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>ref|YP_001436809.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobact
ATCC BAA-894]

gb|ABU75973.1| **G** hypothetical protein ESA_00695 [Enterobacter sakazakii ATCC BA
Length=243]

GENE ID: 5551187 ESA 00695 | pyridoxal phosphate biosynthetic protein PdxJ
[Enterobacter sakazakii ATCC BAA-894]

Score = 437 bits (1124), Expect = 3e-121, Method: Compositional matrix adjust.
Identities = 216/242 (89%), Positives = 227/242 (93%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
        MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
        LRQTL TRMNLEMAVTEEMLA IA ETKPHFCCLVPEKRQEVTTTEGGLDVAGQ DKMRDAC
Sbjct 61 LRQTLHTRMNLEMAVTEEMLTIACTKPHFCCLVPEKRQEVTTTEGGLDVAGQLDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAA+EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
        +RLA AGI VSLFIDAD QI AA VGAP+IEIHTGCIYADA+ DA +A+EL RIAKAAT
Sbjct 121 QRLAAGILVSLFIDADNAQIDA+AVGAPYIEIHTGCIYADAEDDATRARELERIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
        +AAS GLKVNAGHGLTYHNV+AIAA+PEMHELNIGHAIIGRAVM+GLK+AV+EMKRLMLE
Sbjct 181 YAASKGLKVNAGHGLTYHNVQAIAALPEMHELNIGHAIIGRAVMSGLKEAVSEMKRLMLE 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_00822617.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia
ATCC 43970]
Length=243

Score = 397 bits (1020), Expect = 4e-109, Method: Compositional matrix adjust.
Identities = 198/242 (81%), Positives = 212/242 (87%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
        MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI
Sbjct 1 MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
        LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A

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Sbjct  61  LRQTIQTRMNLEMAVTDEMVGIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTVAV  120
Query  121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT  180
          RLA+AGI VSLFIDAD  QI AA  VGAP+IEIHTG YADA TD  +  EL RI KAAT
Sbjct  121  SRLAEAGILVSLFIDADMRQIDAAVTVGAPYIEIHTGAYADATTDLARQAEIVRITKAAT  180
Query  181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +AAS GLKVNAGHGLTYHNV+ IAA+PE+HELNIGHAIIG+AVMTGL AV+EMK LM E
Sbjct  181  YAASKGLKVNAGHGLTYHNVQPIAALPEIHELNIGHAIIGQAVMTGLAAAVSEMKVLMRE  240
Query  241  AR  242
          AR
Sbjct  241  AR  242

```

>ref|ZP_00830259.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 33641]
Length=243

Score = 394 bits (1013), Expect = 3e-108, Method: Compositional matrix adjust.
Identities = 196/242 (80%), Positives = 211/242 (87%), Gaps = 0/242 (0%)

```

Query  1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI  60
          MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct  1  MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI  60
Query  61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC  120
          LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A
Sbjct  61  LRQTIQTRMNLEMAVTDEMVDIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTIAV  120
Query  121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT  180
          RL++AGI VSLFIDAD  QI AA  VGAP+IEIHTG YADA +D  +  EL RIAKAAT
Sbjct  121  SRLSEAGILVSLFIDADMRQIDAAVTVGAPYIEIHTGAYADATSDLARQAEIVRIKAAT  180
Query  181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVM+GL AV EMK LM E
Sbjct  181  YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMSGLATAVTEMKVLMRE  240
Query  241  AR  242
          AR
Sbjct  241  AR  242

```

>ref|YP_001005353.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia e subsp. enterocolitica 8081]

emb|CAL11118.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia enter subsp. enterocolitica 8081]
Length=243

GENE ID: 4716617 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
[Yersinia enterocolitica subsp. enterocolitica 8081] (10 or fewer PubMed links)

Score = 393 bits (1010), Expect = 5e-108, Method: Compositional matrix adjust.
Identities = 196/242 (80%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query  1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI  60
          MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct  1  MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI  60
Query  61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC  120
          LR+T+ TRMNLEMAVT+EM+ IA E PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A
Sbjct  61  LRETIQTRMNLEMAVTDEMVGIAEINPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTVAV  120
Query  121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT  180
          RLA AGI VSLFIDAD  QI AA  VGAP+IEIHTG YADA +D  +  EL RIAKAAT
Sbjct  121  SRLAKAGILVSLFIDADMRQIDAAVAVGAPYIEIHTGAYADATSDLARQAEIVRIKAAT  180
Query  181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +AAS GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVM+GL AV +MK LM E
Sbjct  181  YAASKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMSGLAAAVTDMKVLMRE  240
Query  241  AR  242
          AR
Sbjct  241  AR  242

```

>ref|YP_001400120.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p

IP 31758]

gb|ABS47286.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo
IP 31758]
Length=243

GENE ID: 5386119 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Yersinia pseudotuberculosis IP 31758] (10 or fewer PubMed links)

Score = 392 bits (1006), Expect = 2e-107, Method: Compositional matrix adjust.
Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

```

Query   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60
Sbjct   1      MA+LLLVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60

Query   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC   120
Sbjct   61      LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A     120

Query   121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT   180
Sbjct   121     GRLADVILVSLFIDADFRQIDAAVAAGAPYIEIHTGAYADASTVLERQAEMLRIAKAAT   180

Query   181     FAASLGLKVNAGHGLTYHNVKAIATAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181     YAAGKGLKVNAGHGLTYHNVQPIAALPEMHENLIGHAIIGQAVMTGLATAVDMKVLMLRE   240

Query   241     AR      242
Sbjct   241     AR      242

```

>**ref|NP_668623.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
KIM]

ref|NP_993846.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Microtus str. 91001]

ref|YP_652279.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
Antiqua]
31 more sequence titles

ref|YP_647139.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pesti
Nepal516]

ref|YP_001162910.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
Pestoides F]

ref|ZP_01887420.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
CA88-4125]

ref|YP_001607938.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
Angola]

ref|ZP_02224083.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Orientalis str. F1991016]

ref|ZP_02227818.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Orientalis str. IP275]

ref|ZP_02228990.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Antiqua str. E1979001]

ref|ZP_02238376.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Antiqua str. B42003004]

ref|ZP_02304312.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Antiqua str. UG05-0454]

ref|ZP_02313105.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Orientalis str. MG05-1020]

ref|ZP_02315362.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Mediaevalis str. K1973002]

ref|ZP_02332413.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
FV-1]

ref|YP_001719943.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
YPIII]

ref|YP_002347860.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
CO92]

sp|Q8ZCP4.1|PDXJ_YERPE RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

gb|AAM84874.1|AE013732_6 **G** pyridoxine biosynthesis [Yersinia pestis KIM]

gb|AAS62723.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis
biovar Microtus str. 91001]

gb|ABG17539.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Nepal516]
 gb|ABG14334.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Antiqua]
 emb|CAL21538.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pesti C092]
 gb|ABP39937.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Pestoides F]
 gb|EDM41872.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis CA88-4125]
 gb|ABX88699.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Angola]
 gb|EDR31495.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. IP275]
 gb|EDR37091.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. F1991016]
 gb|EDR44775.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. E1979001]
 gb|EDR50752.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. B42003004]
 gb|EDR56862.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. MG05-1020]
 gb|EDR62700.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. UG05-0454]
 gb|EDR67525.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Mediaevalis str. K1973002]
 gb|ACA67490.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo YPIII]
 Length=243

GENE ID: 1146247 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis KIM] (10 or fewer PubMed links)

Score = 391 bits (1005), Expect = 2e-107, Method: Compositional matrix adjust.
 Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MA+LLLGVNIDHIATLRNARGT YDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
Sbjct	61	LRQTIQTRMNEMAVTDEMVDIACDIKPHFCCLVPEKRQEVTTTEGGLDVAGQVDKMTLAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	YAAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLAAAVTDMKVLRE	240
Query	241	AR	242
Sbjct	241	AR	242

>pdb|3F4N|A **S** Chain A, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|B **S** Chain B, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|C **S** Chain C, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|D **S** Chain D, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|E **S** Chain E, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|F **S** Chain F, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|G **S** Chain G, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|H **S** Chain H, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis
Length=246

Score = 391 bits (1005), Expect = 3e-107, Method: Compositional matrix adjust.
Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 4  MA+LLLGVNIDHIATLRNARGT YDPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 63
        MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
Sbjct 64 LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A 123
        LRQTIQTRMNLEMAVTDEMVDIACDIKPHFCCLVPEKRQEVTTTEGGLDVAGQVDKMTLAV

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 124 RLAD GI VSLFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT 183
        GRLADVILVSLFIDADFRQIDAABAAGAPYIEIHTGAYADASTVLERQAEMLRIKAAT

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 184 +AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E 243
        YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLAAAVTDMKVLNRE

Query 241 AR 242
Sbjct 244 AR 245

```

>ref|ZP_00833834.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 29909]
Length=243

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
Identities = 195/242 (80%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MA+LLLGVNIDHIATLRNARGT YDPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
        MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
Sbjct 61 LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A 120
        LRQTIQTRMNLEMAVTDEMVDIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQLDKMTIIV

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 RL++AGI VSLFID D QI AA VGAP+IEIHTG YADA TD + EL RI KAAT 180
        SRLSEAGILVSLFIDPDMRQIDAABAVGAPYIEIHTGAYADATTDLVRQAEVLVITKAAT

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 +AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E 240
        YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLAAAVTDMKVLNRE

Query 241 AR 242
Sbjct 241 AR 242

```

>ref|ZP_00827187.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 43969]
Length=243

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
Identities = 195/242 (80%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MA+LLLGVNIDHIATLRNARGT YDPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
        MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
Sbjct 61 LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A 120
        LRQTIQTRMNLEMAVTDEMVGIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTIIV

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 RLA+AGI VSLFIDAD QI AA VGAP+IEIHTG YADA TD + EL RI KAAT 180
        SRLAEAGILVSLFIDADMRQIDAABVTGAPYIEIHTGAYADAITDLARQAEVLVITKAAT

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 +AAS GLKVNAGHGLTYHNV+ IAA+PE+ ELNIGHAIIG+AVMTGL AV +MK LM E 240
        YAASKGLKVNAGHGLTYHNVQPIAALPEIQELNIGHAIIGQAVMTGLAAAVGDMKVLNRE

```


Query 241 AR 242
 AR
 Sbjct 241 AR 242

>ref|YP_071394.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseu
 IP 32953]
 ref|YP_001873412.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
 PB1/+]
 sp|Q3V7P0.1|PDXJ YERPS RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 emb|CAH22125.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseud
 IP 32953]
 gb|ACC89955.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo
 PB1/+]
 Length=243

GENE ID: 2956225 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
 [Yersinia pseudotuberculosis IP 32953] (10 or fewer PubMed links)

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
 Identities = 196/242 (80%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Sbjct	1	MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC	120
		LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM	
Sbjct	61	LRQTIQTRMNLEMAVTDEMVDIACDIKPHFCCLVPEKRQEVTTTEGGLDVAGQVDMKMTLVV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		RLAD GI VSLFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT	
Sbjct	121	GRLADVGLVSLFIDADFRQIDAAVAAGAPYIEIHTGAYADASTVLERQAELMRIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E	
Sbjct	181	YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLATAVTDKMLMRE	240
Query	241	AR 242	
		AR	
Sbjct	241	AR 242	

>ref|YP_051364.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Pectobacteriu
 atrosepticum SCRI1043]
 sp|Q3V7N3.1|PDXJ ERWCT RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 emb|CAG76173.1| **G** pyridoxal phosphate biosynthetic protein [Pectobacterium atro
 SCRI1043]
 Length=243

GENE ID: 2882129 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
 [Pectobacterium atrosepticum SCRI1043] (10 or fewer PubMed links)

Score = 390 bits (1001), Expect = 7e-107, Method: Compositional matrix adjust.
 Identities = 194/242 (80%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		MAELLLGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRDVRI	
Sbjct	1	MAELLLGVNIDHIATLRNARGTPYPDPVQAAAFVAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC	120
		LR+TL TRMNLEMAVTEEML IA E KPHFCCLVPEKRQEVTTTEGGLDVAGQ++K+ +A	
Sbjct	61	LRQLQTRMNLEMAVTEEMLNIAACEVKPHFCCLVPEKRQEVTTTEGGLDVAGQKEKIDNAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		RL+ A I VSLFIDAD+ QI AA GA +IEIHTG YADA D + E RI AAT	
Sbjct	121	ARLSQANILVSLFIDADKRQIDAAVASGAAYIEIHTGAYADAPDDETRQHEFERIRDAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+AA+ GLKVNAGHGLTYHNV IAA+PEMHELNIGHAIIGRAV++GLKDAVAEMK LM E	
Sbjct	181	YAAAKGLKVNAGHGLTYHNVLPFAALPEMHELNIGHAIIGRAVISGLKDAVAEMKSLMRE	240
Query	241	AR 242	
		AR	
Sbjct	241	AR 242	

>ref|YP_001479890.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Serratia p 568]

gb|ABV42762.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Serratia protea 568]
Length=243

GENE ID: 5606405 Spro_3666 | pyridoxal phosphate biosynthetic protein PdxJ [Serratia proteamaculañs 568]

Score = 382 bits (981), Expect = 1e-104, Method: Compositional matrix adjust.
Identities = 192/242 (79%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQQRDKMRDAC	120
Sbjct	61	LRQT+ TRMNLEMAVT+EML IA+E KPHFCCLVPEKR+EVTTTEGGLDVAGQ+DKM A	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	++LA AGI VSLFID D QI AA VGAP+IEIHTG YA+A+ + EL RIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	+AA GLKVNAGHGLTYHNV+ IAA+PEMHENLIGHAIIG+AVM GL AV +MK LM E	240
Query	241	AR	242
Sbjct	241	AR	242

>ref|YP_455464.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Sodalis gloss str. 'morsitans']

dbj|BAE75059.1| **G** pyridoxal phosphate biosynthetic protein [Sodalis glossinidius str. 'morsitans']
Length=243

GENE ID: 3866528 SG1784 | pyridoxal phosphate biosynthetic protein PdxJ [Sodalis glossinidius str. 'morsitans'] (10 or fewer PubMed links)

Score = 381 bits (978), Expect = 3e-104, Method: Compositional matrix adjust.
Identities = 187/242 (77%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	M+ELLLGVNIDHIATLRNARG A+PDPVQAAAFIAEQAGADGITVHLREDRRHITDRDV++	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQQRDKMRDAC	120
Sbjct	61	LR+T+ TRMNLEMAVTEEM++IA + PHFCCLVPEKRQEVTTTEGGLDVAGQ DK+R A	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	L+ AGIQVSLFIDADE QI AAA+VGAP+IEIHTG YADA + +A E ARI + A	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	FA LGLKVNAGHGL YHNVK +AA+ +M ELNIGHAI RAV+ GL DAV +MKRLM E	240
Query	241	AR	242
Sbjct	241	AR	242

>ref|NP_930557.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Photorhabdus subsp. laumondii TT01]

sp|Q7N1X8.1|PDXJ PHOLL RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
emb|CAE15711.1| **G** Pyridoxal phosphate biosynthetic protein PdxJ (PNP synthase) [Photorhabdus luminescens subsp. laumondii TT01]
Length=243

GENE ID: 2803349 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Photorhabdus luminescens subsp. laumondii TT01] (10 or fewer PubMed links)

Score = 376 bits (966), Expect = 7e-103, Method: Compositional matrix adjust.
Identities = 184/242 (76%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MAE+LLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRHITDRDV +
Sbjct 1  MAEVLGGVNIDHIATVRNARGTHYPDPVQAAFVAEQAGADGITIHLREDRRHITDRDVEL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          L++T+ TRMNLEMAVT+EM+ IA KP FCCLVPEKRQEVTTTEGGLDV GQ+DK+ A
Sbjct 61  LKKTIQTRMNLEMAVTDEMVDIACRIKPEFCCLVPEKRQEVTTTEGGLDVIGQKDKVAAAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          KRL+DAGI VSLFIDA+ QI AA EVGAFFIEIHTG YADAK + EQ +E RI AAT
Sbjct 121 KRLSDAGILVSLFIDAHEHRQIDAANEVGAFFIEIHTGAYADAKNEVEQEKEFHRIKAAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AAS GL VNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRAV +GL AVA+MK M +
Sbjct 181 YAASKGLTVNAGHGLTYHNVQRIALPEIYELNIGHAIIGRAVFSGLTAAVADMKTQMRK 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|YP_855346.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas hydrophila subsp. hydrophila ATCC 7966]

gb|ABK38566.1| G pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
Length=245

GENE ID: 4487304 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Aeromonas hydrophila subsp. hydrophila ATCC 7966] (10 or fewer PubMed links)

Score = 376 bits (965), Expect = 9e-103, Method: Compositional matrix adjust.
Identities = 187/242 (77%), Positives = 203/242 (83%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+E+ LGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRDV I
Sbjct 1  MSEIYLGVNIDHIATLRNARGTQYPDPVQAAFVAEQAGADGITVHLREDRRHITDRDVEI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          LRQT+ TRMNLEMAVTEEM+ IA +PHF CLVPEKR EVTTTEGGLDVAGQ DK+ DA
Sbjct 61  LRQTIQTRMNLEMAVTEEMIGIACRIQPHFVCLVPEKRTEVTTTEGGLDVAGQLDKVTDVAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RL+ G QVSLFIDAD QI AAAE GAPFIEIHTG YADA TDAE+ E RIA A+
Sbjct 121 ARLSAVGAQVSLFIDADPLQIDAAAESGAPFIEIHTGRYADATTDAAERNAEFKRIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGL YHNVKAIAAIPE++ELNIGHAIIGRA GL AV++M+ LM E
Sbjct 181 YAAGKGLKVNAGHGLHYHNVKAIAAIPELYELNIGHAIIGRAAFDGLAKAVSDMRLLMQE 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_03318787.1| hypothetical protein PROVALCAL_01725 [Providencia alcalifaciens DSM 30120]

gb|EEB46268.1| hypothetical protein PROVALCAL_01725 [Providencia alcalifaciens DSM 30120]
Length=243

Score = 373 bits (958), Expect = 7e-102, Method: Compositional matrix adjust.
Identities = 180/242 (74%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRHITDRDV +
Sbjct 1  MAELLLGVNIDHIATVRNARGTQYPDPVQAAFVAEQAGADGITIHLREDRRHITDRDVEL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          L +T+ TRMNLEMAVTEEM+ IA KP +CCLVPEKR+EVTTTEGGLDVAGQ+ K+ A
Sbjct 61  LNKTIQTRMNLEMAVTEEMIDIACRIKPTYCCLVPEKREEVTTTEGGLDVAGQKQKVAFAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

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Sbjct 121 KRL DAGI VSLFIDAD +QI AA E GAPFIEIHTG YADAKT+ EQ E RI +
KRLTDAGILVSLFIDADHKKIDAAQECGAPFIEIHTGAYADAKTEQEQELEFRIRRDGVS 180
Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AA G+KVNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRA+ +GL AV++MK L++E
Sbjct 181 YAAGGIKVNAGHGLTYHNVQRI AALPEIYELNIGHAIIGRALFSGLSQAVSDMKNLLIE 240
Query 241 AR 242
AR
Sbjct 241 AR 242

```



>ref|ZP_02961267.1| hypothetical protein PROSTU_03281 [Providencia stuartii ATCC 25827]
 gb|EDU60077.1| hypothetical protein PROSTU_03281 [Providencia stuartii ATCC 25827]
 Length=243

Score = 373 bits (957), Expect = 7e-102, Method: Compositional matrix adjust.
 Identities = 182/242 (75%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRD+ +
Sbjct 1 MAELLLGVNIDHIATVRNARGTQYPDPVQAAFFVAEQAGADGITVHLREDRRHITDRDIEL 60
Query 61 LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC 120
L++T+ TRM NLEMAVTEEM+ IA KP FCCLVPEKR+EVTTTEGGLDVAGQ K+ DA
Sbjct 61 LKETIQTRM NLEMAVTEEM INIACRVKPAFCCLVPEKREEVTTTEGGLDVAGQLPKITDAV 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAPFIEIHTG CYADAKTDAEQ AQELARI AKAAT 180
KRL+AGIQVSLFIDAD QI AA GAPFIEIHTG YADAKT+ EQ E RI
Sbjct 121 KRLTEAGIQVSLFIDADHTQIDAAQAAGAPFIEIHTGAYADAKTEQEQEIEYRRIRRDGVA 180
Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AA GLKVNAGHGLTYHNV+ IA +PE++ELNIGHAIIGRA+ +GL +AVA+MK+L+ E
Sbjct 181 YAAGKGLKVNAGHGLTYHNVQRI ALLPEIYELNIGHAIIGRALFSGLANAVADMKKLLRE 240
Query 241 AR 242
AR
Sbjct 241 AR 242

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>ref|YP_002151612.1|  pyridoxal phosphate biosynthetic protein [Proteus mirabilis]
 emb|CAR43908.1|  pyridoxal phosphate biosynthetic protein [Proteus mirabilis H]
 Length=243



GENE ID: 6803577 **pdxJ** | pyridoxal phosphate biosynthetic protein
 [Proteus mirabilis HI4320] (10 or fewer PubMed links)

Score = 372 bits (956), Expect = 1e-101, Method: Compositional matrix adjust.
 Identities = 181/242 (74%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
M+++LLGVNIDHIATLRNARGT YPDPVQAAFI AEQAGADGIT+HLREDRRHITDRD+ +
Sbjct 1 MSDILLGVNIDHIATLRNARGTTYPDPVQAAFI AEQAGADGITIHLREDRRHITDRDML 60
Query 61 LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC 120
+ QT+ TR+ NLEMAVTEEM+ IA +T+P FCCLVPEKRQEVTTTEGGLDV G +K+ DA
Sbjct 61 ISQTVQTRLNLEMAVTEEM IEIACQTQPDFFCCLVPEKRQEVTTTEGGLDVVGNEEKVADAI 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAPFIEIHTG CYADAKTDAEQ AQELARI AKAAT 180
KRL+ AGI+VSLFID D EQI AA VGAPFIEIHTG YADA+ + Q +E RI A T
Sbjct 121 KRLSLAGIKVSLFIDPDHEQINAADRVGAPFIEIHTGAYADAEDAQAQEKEFVRIRDAVT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AAS GLKVNAGHGL YHNV+ IAA+PE++ELNIGHAIIGRAV +GL AV EMKRLM E
Sbjct 181 YAASKGLKVNAGHGLHYHNVQRI AALPELYELNIGHAIIGRAVFSGLAPAVEEMKRLMRE 240
Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|YP_001143199.1|  pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas subsp. salmonicida A449]
 gb|AB091451.1|  pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas salmo subsp. salmonicida A449]

Length=245

GENE ID: 4996852 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Aeromonas salmonicida subsp. salmonicida A449]

Score = 372 bits (954), Expect = 2e-101, Method: Compositional matrix adjust.
Identities = 184/242 (76%), Positives = 201/242 (83%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+E+ LGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRRHITDRDV I	
Sbjct	1	MSEIYLGVNIDHIATLRNARGTQYPDPVQAAFVAEQAGADGITVHLREDRRRHITDRDVEI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LRQT+ TRMNLEMAVTEEM+ IA KPHF CLVPEKR EVTTTEGGLDVAGQ DK+ DA	
Sbjct	61	LRQTIQTRMNLEMAVTEEMIGIACRIKPHFVCLVPEKRTEVTTTEGGLDVAGQLDKITDAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		RL+ G QVSLFIDAD QI AAA+ GAPFIEIHTG YADA TD ++ E RIA A+	
Sbjct	121	TRLSAVGAQVSLFIDADPLQIDAAADSGAPFIEIHTGRYADATTDTRNAEFKRIAAGAS	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+AA GLKVNAGHGL YHNVKAIAAIP E++ELNIGHAIIGRA GL AV++M+ LM E	
Sbjct	181	YAAGKGLKVNAGHGLHYHNVKAIAAIP ELYELNIGHAIIGRAAFDGLTKAVSDMRLLMQE	240
Query	241	AR	242
		R	
Sbjct	241	VR	242

>ref|ZP_03315319.1| hypothetical protein PROVRUST_02121 [Providencia rustigianii DSM 454T]

gb|EEB38919.1| hypothetical protein PROVRUST_02121 [Providencia rustigianii DSM 4541]

Length=243

Score = 367 bits (942), Expect = 4e-100, Method: Compositional matrix adjust.
Identities = 178/242 (73%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		MAELL LGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRRHITDRDV +	
Sbjct	1	MAELL LGVNIDHIATVRNARGTQYPDPVQAAFVAEQAGADGITIHLREDRRRHITDRDVEL	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		L QT+ TRMNLEMAVT+EM+ IA KP +CCLVPEKR+EVTTTEGGLDVAGQ+ K+ A	
Sbjct	61	LNQTIQTRMNLEMAVTDEMIDIACRIKPTYCCLVPEKREEVTTTEGGLDVAGQKQKVAAAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		KRL ++GI VSLFIDAD EQI AA E GAPFIEIHTG YADAKT+ Q E RI	
Sbjct	121	KRLTESGILVSLFIDADHEQIDAAQECGAPFIEIHTGAYADAKTEQAQEIEFRIRIDGVK	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+AA G+KVNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRA+ +GL AV++MK+L+ E	
Sbjct	181	YAAGKGIKVNAGHGLTYHNVQRI AALPEIYELNIGHAIIGRALFSGLAQAVSDMKQLLTE	240
Query	241	AR	242
		AR	
Sbjct	241	AR	242

>ref|ZP_01262022.1| pyridoxal phosphate biosynthetic protein [Vibrio alginolytic 12G01]

gb|EAS74655.1| pyridoxal phosphate biosynthetic protein [Vibrio alginolyticus 12G01]

Length=244

Score = 361 bits (926), Expect = 3e-98, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDVRI	
Sbjct	1	MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LR+T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ +K++ A	
Sbjct	61	LRETIQTRMNLEMAVTDEMIEIALQTKPEFVCLVPEKREELTTEGGLDVVGQLEKIKAAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		K+L DAGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA T+ EQ EL +IA A+	
Sbjct	121	KKLTDAIKVSLFIDADRQQIEAAKCGAPFIELHTGHYADATTEDEQQQELKKIAAGAS	180

```

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL AVA+MK LM+E
Sbjct 181 YAHDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLNKAVADMKALMIE 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|ZP_03385196.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. M223]
Length=192

Score = 360 bits (925), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 179/192 (93%), Positives = 183/192 (95%), Gaps = 0/192 (0%)

```


Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTDYDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60


Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC
Sbjct 61 LRQTLHTRMNLEMAVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
RLA AGIQVSLFIDADE QI AAAEEVGAPFIEIHTGICYA+A+TDAEQA+ELARIA AAT
Sbjct 121 ARLAAAGIQVSLFIDADERQINAAAEEVGAPFIEIHTGICYANAETDAEQAKELARIAAAT 180

Query 181 FAASLGLKVNAG 192
AA LGLKVNAG
Sbjct 181 LAARLGLKVNAG 192

```

>ref|YP_205467.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri ES114]

sp|Q5E317.1|PDXJ VIBF1  RecName: Full=Pyridoxine 5'-phosphate synthase; Short=pyridoxine 5'-phosphate synthase [Vibrio fischeri ES114]
Length=243

GENE ID: 3279332 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri ES114] (10 or fewer PubMed links)

Score = 360 bits (924), Expect = 5e-98, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
M+ +LLGVNIDH+ATLRNARGT YPDPV AA IAE+AGA GIT+HLREDRRHI DRDVRI
Sbjct 1 MSSILLGVNIDHVATLRNARGTKYPDPVHAAEIAERAGAAGITIHLEDRRRHIKDRDVRI 60



Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
LR+TL TRMNLEMAVT+EM+ IA+ETKP F CLVPEKR+E+TTEGGL+V+GQ +K++ A
Sbjct 61 LRETLLQTRMNLEMAVTDEMVGIALETKPEFVCLVPEKREELTTEGGLNVSGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
++L +AGI+VSLFIDAD+EQI AA E GAPFIE+HTG YADA+T+ Q EL +IA A+
Sbjct 121 QKLTEAGIKVSLFIDADKEQIDAAVECGAPFIELHTGAYADAETEEAQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRA+ GL+ AVA+M R+ML
Sbjct 181 YAASKGLIVNAGHGLTYHNVEAIAALPEIYELNIGHSIMGRAMFDGLEKAVADMHRIMLG 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|YP_002073491.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio sp. Ex25]
gb|EDN55839.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio sp. Ex25]
Length=243

GENE ID: 6654483 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio sp. Ex25]

Score = 358 bits (920), Expect = 1e-97, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ + LGVNIDHIATLRNARGT YDPDV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHILDRDVRI 60

Query 61 LRQTLDRMNLMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
      LR+T+ TRMNLMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGLDV GQ +K++ A
Sbjct 61 LRETIQTRMNLMAVTDEMVEIALQTQPEFVCLVPEKREELTTEGGLDVVGQLEKIKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      K+L DAGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA T+ EQ EL +IA A+
Sbjct 121 KKLTDAGIKVSLFIDADRQQIEAAKKGAPFIELHTGHYADATTEDEQQAELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL AVA+MK LM+E
Sbjct 181 YAHDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLNKAVADMKALMIE 240

Query 241 AR 242
      AR
Sbjct 241 AR 242

```

>ref|YP_002156883.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fis MJ11]

gb|ACH66587.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri MJ11]

Length=243

GENE ID: 6806102 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri MJ11]

Score = 358 bits (919), Expect = 2e-97, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDH+ATLRNARGT YDPDV AA IAE+AGA GIT+HLREDRRHI DRDVRI
Sbjct 1 MSSILLGVNIDHVATLRNARGTKYPDPVHAAEIAERAGAAGITIHLEDRRHILKDRDVRI 60

Query 61 LRQTLDRMNLMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
      LR+TL TRMNLMAVT+EM+ IA+ETKP F CLVPEKR+E+TTEGGL+V+GQ +K++ A
Sbjct 61 LRETLLQTRMNLMAVTDEMVGIALETKPEFVCLVPEKREELTTEGGLNVSGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      ++L +AGI+VSLFIDAD++QI AA E GAPFIE+HTG YADA+T+ Q EL +IA A+
Sbjct 121 QKLTEAGIKVSLFIDADKKQIDAAVECGAPFIELHTGAYADAETEEAQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRA+ GL+ AV++M R+ML
Sbjct 181 YAASKGLIVNAGHGLTYHNVVEAIAALPEIYELNIGHSIMGRAMFDGLEKAVSDMHRIMLG 240

Query 241 AR 242
      AR
Sbjct 241 AR 242

```

>ref|ZP_03400922.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Typhi str. AG3].
Length=191

Score = 357 bits (916), Expect = 5e-97, Method: Compositional matrix adjust.
Identities = 176/191 (92%), Positives = 183/191 (95%), Gaps = 0/191 (0%)

```

Query 53 ITDRDVRILRQTLDRMNLMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ 112
      +TDRDVRILRQTL TRMNLMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQ
Sbjct 1 MTDRDVRILRQTLHTRMNLMAVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQ 60

Query 113 RDKMRDACKRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQEL 172
      RDKMRDAC RLA AGIQVSLFIDADE QI AAAEEVGAPFIEIHTGCIY+A+TDAEQA+EL
Sbjct 61 RDKMRDACARLAAAGIQVSLFIDADERQINAAAEEVGAPFIEIHTGCIYANAETDAEQAKEL 120

Query 173 ARIAKAATFAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVA 232
      ARIA AAT AA LGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVMTGLK+AVA
Sbjct 121 ARIASAATLAARLGLKVNAGHGLTYHNVKAIAALPEMHELNIGHAIIGRAVMTGLKEAVA 180

Query 233 EMKRLMLEARG 243
      EMKRLMLEARG
Sbjct 181 EMKRLMLEARG 191

```


>ref|NP_760465.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio vulnif CMCP6]
 ref|NP_935621.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio vulnif YJ016]
 sp|Q8DC73.1|PDXJ_VIBVU RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 sp|Q7MHP1.1|PDXJ_VIBVY **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
 gb|AAO09992.1|AE016802_35 **G** Pyridoxal phosphate biosynthesis protein [Vibrio vu
 dbj|BAC95592.1| **G** pyridoxal phosphate biosynthesis protein [Vibrio vulnificus Y
 Length=243

GENE ID: 1178481 VV1 1568 | pyridoxal phosphate biosynthetic protein PdxJ
 [Vibrio vulnificus CMCP6] (10 or fewer PubMed links)

Score = 356 bits (914), Expect = 9e-97, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M+ + LGVNIDH+ATLRNARGT YDPDV AA +AE+AGADGIT+HLREDRRHITDRDVRI	
Sbjct	1	MSSIY LGVNIDHVATLRNARGTKYPDPVHAAEVAERAGADGITIHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDVAG DK++ A	
Sbjct	61	LRET LQTRMNLEMAVTDEMIEIALKTQPEYVCLVPEKREELTTEGGLDVAGHLDKIKAAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		++L AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA T+A+Q EL +IA A+	
Sbjct	121	EKLTAAGIKVSLFIDADREQIDAACACGAPFIELHTGHYADAATEADQLDELKKIAAGAS	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+AA LG+ VNAGHGLTYHNV IAA+PE++ELNIGHAIIGRAV GL AVA+MK +M+	
Sbjct	181	YAADLGITVNAGHGLTYHNVAIPAAALPEIYELNIGHAIIGRAVFDGLHKAVADMKAIMVA	240
Query	241	AR	242
		AR	
Sbjct	241	AR	242

>ref|YP_131204.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Photobacteriu profundum SS9]
 sp|Q3V7I6.1|PDXJ PHOPR RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 emb|CAG21402.1| **G** putative pyridoxal phosphate biosynthetic protein PdxJ [Photob profundum SS9]
 Length=243

GENE ID: 3123572 PBPA3086 | pyridoxal phosphate biosynthetic protein PdxJ
 [Photobacterium profundum SS9] (10 or fewer PubMed links)

Score = 355 bits (912), Expect = 1e-96, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M +LLGVNIDHIATLRNARGT YDPDV AA +AE+AGADGITVHLREDRRHI DRDVRI	
Sbjct	1	MNNILLGVNIDHIATLRNARGTRYPDPVHAAEVAERAGADGITVHLREDRRHINDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		L++T+ TRMNLEMAVT+EM++IA++TKP F CLVPEKR+E+TTEGGLDVAGQ +K++ A	
Sbjct	61	LKETIQTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGLDVAGQLEKIKAAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		++L DAGI+VSLFIDAD QI A GAPF+E+HTG YADA+T+ Q EL +IA AAT	
Sbjct	121	QKLT DAGIKVSLFIDADRAQIDATLACGAPFVELHTGHYADAETEEAQQAELEKIASAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+II RA GL AVA+MK ML+	
Sbjct	181	YAHGLGIKVNAGHGLTYHNVKPIAALPELYELNIGHSIISRAAFDGLNKAVADMKVEMLD	240
Query	241	AR	242
		AR	
Sbjct	241	AR	242

>ref|ZP_01816562.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrionales b SWAT-3]
 gb|EDK26047.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrionales bacte SWAT-3]

Length=245

Score = 354 bits (909), Expect = 3e-96, Method: Compositional matrix adjust.
 Identities = 171/243 (70%), Positives = 204/243 (83%), Gaps = 0/243 (0%)

```


Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ +LLGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MSSILLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHIVDRDVRI 60


Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
          L +T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGGLDV GQ DK++ A
Sbjct 61  LAETIQTRMNLEMAVTDEMVDQIALDTKPEFVCLVPEKREELTTEGGGLDVVGQLDKIKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          ++L++AGI+VSLFIDAD EQI AA GAPFIE+HTG YADAKT+ +Q EL +IA A+
Sbjct 121 QKLSEAGIKVSLFIDADREQIDAACACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRAV GL AVA+MK +M
Sbjct 181 YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET 240

Query 241 ARG 243
          AR
Sbjct 241 ARN 243
  
```

>ref|YP_001906938.1|  Pyridoxal phosphate biosynthetic protein (PNP synthase) [tasmaniensis Et1/99]

emb|CA096041.1|  Pyridoxal phosphate biosynthetic protein (PNP synthase) [Erwinia tasmaniensis Et1/99]
 Length=243

GENE ID: 6299767 pdxJ | Pyridoxal phosphate biosynthetic protein (PNP synthase) [Erwinia tasmaniensis Et1/99]

Score = 354 bits (908), Expect = 4e-96, Method: Compositional matrix adjust.
 Identities = 186/243 (76%), Positives = 205/243 (84%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          MAELLLGVNIDH+AT+RNARGT YPDPVQAAAF++EQAGADGITVHLREDRRHI DRDVRI
Sbjct 1  MAELLLGVNIDHVATVRNARGTNYPDPVQAAAFVSEQAGADGITVHLREDRRRHINDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
          LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKR+EVTTTEGGGLDVAGQ DK+ A
Sbjct 61  LRQTIQTRMNLEMAVTDEMVDIACEIQPHFCCLVPEKREEVTTTEGGGLDVAGQLDKVTA AV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          KRL DAG+ VSLFIDAD QI AA GAP+IEIHTG YA+A + ELARIA AAT
Sbjct 121 KRLNDAGVLVSLFIDADRGQIDAABAAGAPYIEIHTGAYAEAPEGLARDELTARIAAAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGLTYHNV IAA+PEM ELNIGHAIIGRAV +GL AV EMK+L+
Sbjct 181 YAAGKGLKVNAGHGLTYHNVLPAAALPEMVELNIGHAIIGRAVFSGLAAAVQEMKQLLRA 240

Query 241 ARG 243
          ARG
Sbjct 241 ARG 243
  
```

>ref|ZP_01161526.1| pyridoxal phosphate biosynthetic protein [Photobacterium sp. SKA34]

gb|EAR54737.1| pyridoxal phosphate biosynthetic protein [Photobacterium sp. SKA34]
 Length=243

Score = 353 bits (906), Expect = 7e-96, Method: Compositional matrix adjust.
 Identities = 168/243 (69%), Positives = 208/243 (85%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M +LLGVNIDHIATLRNARGT+YPDPV AA +AE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MNNILLGVNIDHIATLRNARGTSYPDPVHAAEVAERAGADGITIHLREDRRRHINDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVT+EM+AIA++ KP + CLVPEKR+E+TTEGGGLDV+GQ +K++ A
Sbjct 61  LRETIQTRMNLEMAVTDEMVAIALDVKPEYVCLVPEKREELTTEGGGLDVSGQLEKVKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          ++L AGI+VSLFIDAD QI AA GAPFIE+HTG YA+AKT+ Q EL ++A A+
  
```

```

Sbjct 121 EKLTAAGIKVSLFIDADRAQIDAAHACGAPFIELHTGQYAEAKTEEAQLDELKKVAAGAS 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIIP+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E 240
          +A +LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E
Sbjct 181 YAHNLGIKVNAGHGLTYHNVKLI AALPELYELNIGHSIMGRAMFDGLEKSVADMRLLMQE 240
Query 241 ARG 243
          ARG
Sbjct 241 ARG 243

```

>ref|YP_002127690.1| **G** pyridoxal phosphate biosynthetic protein [Alteromonas mac
'Deep ecotype']

gb|ACG67696.1| **G** pyridoxal phosphate biosynthetic protein [Alteromonas macleodi
'Deep ecotype']
Length=250

GENE ID: 6778911 MADE 03404 | pyridoxal phosphate biosynthetic protein
[Alteromonas macleodii-'Deep ecotype'] (10 or fewer PubMed links)

Score = 353 bits (905), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLRNARGT YDPV AA IAE+AGADGITVHLREDRRHI DRDVRI
Sbjct 6 MSTILLGVNIDHIATLRNARGTHYPDPVHAADIAERAGADGITVHLREDRRHIKDRDVRI 65
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          L QT++TR+NLEMAVT+EMLAIA E KP FCCLVPEKR+E+TTEGGLDVAG D ++ AC
Sbjct 66 LAQTINTRLNLEMAVTDEMLAIAEEVKPVFCCLVPEKREELTTEGGLDVAGNVDNKAAC 125
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA+A I VSLFIDAD+ QI AAA AP+IEIHTG YA+A ++ Q +ELAR+ +
Sbjct 126 DRLANANILVSLFIDADKAQIDAAAACNAPYIEIHTGQYAEATSEEAQQEELARLVEGIE 185
Query 181 FAASLGLKVNAGHGLTYHNVKAIIP+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E 240
          +A SLGLKVNAGHGL YHNVK IAAIP++ ELNIGH+I+GRA+ GL AVA+M++LMLE
Sbjct 186 YADSLGLKVNAGHGLHYHNVKPIAAIPQLIELNIGH+I+GRA+ GL AVA+M++LMLE 245
Query 241 AR 242
          AR
Sbjct 246 AR 247

```

>ref|ZP_01870295.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio shilon
AK1]

gb|EDL51107.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio shilonii
AK1]
Length=244

Score = 352 bits (904), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 170/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLG+NIDHIATLRNARGT YDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSILLGINIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHILDRDVRI 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LR+TL TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGLDV GQ +K++ A
Sbjct 61 LRETQLQTRMNLEMAVTDEMIDIALKTQPEFVCLVPEKREELTTEGGLDVKGQLEKIKAAAT 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L+ AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA+T+ +Q EL +IA A+
Sbjct 121 EKLSAAGIKVSLFIDADREQIDAAKAAGAPFIELHTGHYADAETEEDQQDELKKIAAGAS 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIIP+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E 240
          +AA +G+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRA+ GL AVA+MK +M
Sbjct 181 YAADIGITVNAGHGLTYHNVAPIAALPEIYELNIGH+I+GRA+ GL AVA+MK +M 240
Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|YP_588729.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Baumannia cic
str. Hc (Homalodisca coagulata)]

gb|ABF13930.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Baumannia cicad

str. Hc (Homalodisca coagulata)]
Length=243

GENE ID: 4056676 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Baumannia cicadellinicola str. Hc (Homalodisca coagulata)]
(10 or fewer PubMed links)

Score = 352 bits (904), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 166/243 (68%), Positives = 201/243 (82%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ LLL VNIDHIATLRNARGT +PDPVQAAAFIAE AGADGITVHLREDRRHI DRDV +	
Sbjct	1	MSRLLLNVDNIDHIATLRNARGTTWDPVQAAAFIAEDAGADGITVHLREDRRRHINDRDVMT	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC	120
		LRQT+ TRMNLEMA+T++M+AIA +P CCLVPEKROE+TTEGGGLDVA Q+ K+ +A	
Sbjct	61	LRQTIKTRMNLEMAITDDMIAIACSVRPDLCLVPEKROELTTEGGGLDVAQQKKKISNAI	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		L++AGI VSLFIDAD++QI+AAAE+G+P+IEIHTGICYA+A+ + E EL RI +AA	
Sbjct	121	YLLSEAGIMVSLFIDADKQQIEAAAEIGSPYIEIHTGICYANARNNTECIAELERIRQAAD	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A SLGLKVNAGHGLTYHNV+ IA + +HELNIGH+II RA+++GL A+ M L+	
Sbjct	181	YATSLGLKVNAGHGLTYHNVQDIAMLSFIHELNIGHSSIISRAIISGLNQAIINMINLLHN	240
Query	241	ARG 243	
		AR	
Sbjct	241	ARS 243	

>ref|ZP_01220096.1| pyridoxal phosphate biosynthetic protein [Photobacterium pro 3TCK]
>gb|EAS43446.1| pyridoxal phosphate biosynthetic protein [Photobacterium profund 3TCK]
Length=243

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M +LLGVNIDHIATLRNARGT YPDPV AA +AE+AGADGITVHLREDRRHI DRDVRI	
Sbjct	1	MNNILLGVNIDHIATLRNARGTRYDPVHAAEVAERAGADGITVHLREDRRRHINDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC	120
		L++T+ TRMNLEMAVT+EM++IA++TKP F CLVPEKR+E+TTEGGGLDVAGQ +K++ A	
Sbjct	61	LKETIQTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGGLDVAGQLEKIKAAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		++L AGI+VSLFIDAD QI A GAPF+E+HTG YADA+T+ Q EL +IA AAT	
Sbjct	121	QKLTAAGIKVSLFIDADRAQIDATLACGAPFVELHTGHYADAETEEAQQAEQELDKIASAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+IIGRA GL AVA+MK +L+	
Sbjct	181	YAHGLGIKVNAGHGLTYHNVKPIAALPELYELNIGHSSIIGRAAFDGLNKAVADMKVEVLD	240
Query	241	AR 242	
		AR	
Sbjct	241	AR 242	

>ref|YP_002263870.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Aliivibrio LFI1238]

>emb|CAQ80206.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Aliivibrio sal LFI1238]
Length=243

GENE ID: 6988220 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio salmonicida LFI1238]

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ +LLGVNIDH+ATLRNARGT YPDPV AA IAE+AGA GIT+HLREDRRHI DRDVRI	
Sbjct	1	MSSILLGVNIDHVATLRNARGTKYPDPVHAAEIAERAGAAGITIHLEDRRRHIKORDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC	120

```

Sbjct 61 LR+TL TRMNLEMAVT+EM+ IA+ET+P F CLVPEKR+E+TTEGGL+V GQ +K++ A .
LRETlQTRMNLEMAVTDEMVGIALETQPEFVCLVPEKREELTTEGGLNVVGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
+ L+ AGI+VSLFIDAD QI AA GAPFIE+HTG YADA+T+ + EL +IA AT
Sbjct 121 QTLKAGIKVSLFIDADNAQIDAACVACGAPFIELHTGAYADAETEEAEQIELKKIAAGAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRAV GL+ AVA+M R+ML
Sbjct 181 YAASKGLIVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|ZP_01236135.1| pyridoxal phosphate biosynthetic protein [Vibrio angustum S1
gb|EAS63814.1| pyridoxal phosphate biosynthetic protein [Vibrio angustum S14]
Length=243

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 168/243 (69%), Positives = 207/243 (85%), Gaps = 0/243 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
M +LLGVNIDHIATLRNARGT YDPV AA +AE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MNNILLGVNIDHIATLRNARGTRYDPVHAAEVAERAGADGITIHLREDRRHINDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
LR+T+ TRMNLEMAVT+EM+AIA++ KP + CLVPEKR+E+TTEGGLDVAGQ +K++ A
Sbjct 61 LRETlQTRMNLEMAVTDEMVAIALDVKPEYVCLVPEKREELTTEGGLDVAGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
++L AGI+VSLFIDAD QI AA GAPFIE+HTG YA+A T+ Q+ EL ++A A+
Sbjct 121 EKLTAAGIKVSLFIDADRAQIDAACACGAPFIELHTGQYAEATTEEAQSDDELKKVAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A +LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E
Sbjct 181 YAHNLGIKVNAGHGLTYHNVKPIAALPELYELNIGHSIMGRAMFDGLEKSVADMRLLMQE 240

Query 241 ARG 243
ARG
Sbjct 241 ARG 243

```

>gb|EED26525.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemol
16]
Length=243

Score = 351 bits (901), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 169/242 (69%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
M+ + LGVNIDHIATLRNARGT YDPV AA +AE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEVAERAGADGITIHLREDRRHINDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
LR+T+ TRMNLEMAVT+EM+ IA+ T+P + CLVPEKR+E+TTEGGLDV GQ +K++ A
Sbjct 61 LRETlQTRMNLEMAVTDEMVEIALNTQPEYVCLVPEKREELTTEGGLDVVGQLEKVKAAAT 120


Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
++L++AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA+T+ +Q EL +IA A+
Sbjct 121 QKLSEAGIKVSLFIDADREQIDAACACGAPFIELHTGHYADAETEEEDQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AA LG+ VNAGHGLTYHNV AIAA+PE++ELNIGH+I+GRA GL AVA+MK M+
Sbjct 181 YAADLGITVNAGHGLTYHNVAAIAA+PELYELNIGHSIIGRAAFDGLHKAVADMKAQMVL 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|ZP_01988133.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio harvey
HY01]

ref|YP_001446696.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio har
ATCC BAA-1116]

gb|EDL67174.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio harveyi
HY01]

gb|ABU72469.1| **G** hypothetical protein VIBHAR_03533 [Vibrio harveyi ATCC BAA-111 Length=243]

Score = 350 bits (899), Expect = 4e-95, Method: Compositional matrix adjust.
Identities = 168/242 (69%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ + LGVNIDHIATLRNARGT YDPDV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHILDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGGLDV GQ +K++ A
Sbjct 61  LRETIQTRMNLEMAVTDEMVEIALQTKPEFVCLVPEKREELTTEGGGLDVVGQLEKVKAAAT 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L +AGI+VSLFIDAD +QI AA  GAP+IE+HTG YADA T+ +Q EL +IA A+
Sbjct 121  QKLTEAGIKVSLFIDADRQQIDAACACGAPYIELHTGHYADATTEEDQQDELKKIAAGAS 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL+ +VAEMK +M+
Sbjct 181  YADDLGIIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLEKSVAEMKAIMVA 240

Query 241  AR 242
          AR
Sbjct 241  AR 242

```

>**ref|ZP_01215567.1|** pyridoxal phosphate biosynthetic protein [Psychromonas sp. C
gb|EAS39633.1| pyridoxal phosphate biosynthetic protein [Psychromonas sp. CNPT3 Length=246]

Score = 350 bits (899), Expect = 5e-95, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 197/242 (81%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M++LLLVNIDH+ATLRNARGT YP+P A IAE +GADGIT+HLREDRRHI DRDV I
Sbjct 1  MSKLLLVNIDHVAATLRNARGTCYPEPAHLAIAETSGADGITIHLREDRRHIIDRDVAI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          L QTL TRMNLEMA+T+EM+ IA++TKP F CLVPEKR E+TTEGGGLDVAG DK R A
Sbjct 61  LAQTLQTRMNLEMAITDEMIDIAIKTKPAFVCLVPEKRAELTTEGGGLDVAGALDKTRSAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          +RL AGIQVSLFIDAD+ QI AA  GAP+IE+HTG YADA D QA EL R+A AT
Sbjct 121  QRLTQAGIQVSLFIDADKNQIDAALASGAPYIELHTGKYADALDDMQALELQRVASMAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LGLKVNAGHGL YHNVKAIAA+PE+ ELNIGHAI RA++ GL AV EMKRLM+E
Sbjct 181  YAHGLGLKVNAGHGLNYHNVKAI AALPEI IELNIGHAI IARALVDGLSVAVQEMKRLMIE 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>**ref|ZP_01064680.1|** pyridoxal phosphate biosynthetic protein [Vibrio sp. MED222]
ref|YP_002418187.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Vibrio spl LGP32]
gb|EAQ53969.1| pyridoxal phosphate biosynthetic protein [Vibrio sp. MED222]
emb|CAV19823.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Vibrio splendi LGP32]
Length=245

Score = 349 bits (895), Expect = 1e-94, Method: Compositional matrix adjust.
Identities = 169/242 (69%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLRNARGT YDPDV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MSSILLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHIVDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          L +T+ TRMNLEMAVT+EM+ IA++T P F CLVPEKR+E+TTEGGGLDV GQ +K++ A
Sbjct 61  LAETIQTRMNLEMAVTDEMVIQALDTNPEFVCLVPEKREELTTEGGGLDVVGQLEKIKAAAT 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L+ AGI+VSLFIDAD EQI AA  GAPFIE+HTG YADAKT+ +Q EL +IA A+
Sbjct 121  EKLSAAGIKVSLFIDADREQIDAACACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS 180

```

```

Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRAV GL AVA+MK +M
Sbjct 181 YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>gb|EAZ49556.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae V51]
Length=243

Score = 348 bits (893), Expect = 2e-94, Method: Compositional matrix adjust.
Identities = 172/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ + LGVNIDH+ATLRNARGT+YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDVRI
Sbjct 1 MSSIYLGVNIDHVATLRNARGTSYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI 60



Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDV GQ ++++ A
Sbjct 61 LRETLLQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGLDVLGQLERVKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA
Sbjct 121 EKLTAAGIKVSLFIDADREQIDAAKACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA 180

Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV AIAAIP++ELNIGHAIIGRAV GL AVA+MK +M+
Sbjct 181 YAHDLGITVNAGHGLTYHNVAAIAAIPYELNIGHAIIGRAVFDGLAKAVADMKAIMVA 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|NP_798948.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemolyticus RIMD 2210633]
sp|Q87LP2.1|PDXJ VIBPA RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
dbj|BAC60832.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemolyticus RIMD 2210633]
Length=243

GENE ID: 1190093 VP2569 | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio parahaemolyticus RIMD 2210633] (10 or fewer PubMed links)

Score = 348 bits (892), Expect = 3e-94, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 207/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVTEEM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ DK++ A
Sbjct 61 LRETIQTRMNLEMAVTEEMVEIALKTKPEFVCLVPEKREELTTEGGLDVVGQLDKVKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L +AGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA+T+ EQ EL +IA A+
Sbjct 121 QKLTEAGIKVSLFIDADRQQIEAAKQCGAPFIELHTGHYADAETEEQQAEELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL+ +VAEMK LM+
Sbjct 181 YADDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLEKSVAEMKALMIA 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

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>ref|ZP_00991369.1| pyridoxal phosphate biosynthetic protein [Vibrio splendidus]
gb|EAP93636.1| pyridoxal phosphate biosynthetic protein [Vibrio splendidus 12B0]
Length=245

Score = 347 bits (890), Expect = 4e-94, Method: Compositional matrix adjust.
Identities = 168/242 (69%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
Sbjct 1  MSSILLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHIVDRDVRI 60


Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LAETIQTRMNLEMAVTDEMVMQIALDTNPEFVCLVPEKREELTTEGGLDVVGQLEKIKAAAT 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAEQELARIAKAAT 180
Sbjct 121  EKLSAAGIKVSLFIDAEREQIDAACACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS 180


Query 181  FAASLGLKVNAGHGLTYHNVAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  YADDLGITVNAGHGLTYHNVAIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET 240


Query 241  AR 242
Sbjct 241  AR 242


```


>ref|NP_232087.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar eltor str. N16961]
 ref|ZP_01678308.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 2740-80]
 ref|ZP_01953186.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MAK 757]
 15 more sequence titles

ref|ZP_01957675.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-3]
 ref|ZP_01979577.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-2]
 ref|ZP_01983536.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 623-39]

ref|YP_002066631.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae M010]

ref|YP_002069749.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae RC385]

ref|YP_002174421.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae AM-19226]

sp|Q9KPB5.1|PDXJ VIBCH RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 gb|AAF95600.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar El Tor str. N16961]


gb|EAX57295.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 2740-80]


gb|EAY37632.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MAK 757]

gb|EAY40114.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-3]

gb|EDL71773.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 623-39]

gb|EDM53535.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-2]

gb|EDN11667.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae RC385]

gb|EDN14389.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae AM-19226]
 Length=243

GENE ID: 2613000 VC2458 | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar eltor str. N16961] (10 or fewer PubMed links)

Score = 347 bits (890), Expect = 5e-94, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
Sbjct 1  MSSIYLGVNIDHVATLRNARGTQYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRETLOTRMNLEMAVTDEMVEIALQTOPEYVCLVPEKREELTTEGGLDVLGQLERVKAAT 120

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Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA
Sbjct 121 EKLTAAGIKVSLFIDADREQIDAAKACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A LG+ VNAGHGLTYHNV AIAAIP++ELNIGHAIIGRAV GL AVA+MK +M+
Sbjct 181 YAHDLGITVNAGHGLTYHNVAAIAAIPAIYELNIGHAIIGRAVFDGLAKAVADMKAIMVA 240

Query 241 AR 242
AR
Sbjct 241 AR 242

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>ref|ZP_02196848.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio campbe
AND4]
gb|EDP58079.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio campbellii
AND4]
Length=243

Score = 347 bits (889), Expect = 6e-94, Method: Compositional matrix adjust.
Identities = 166/242 (68%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITHLREDRRRHITDRDVRI 60
M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITHLREDRRRHILDRDVRI 60



Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
LR+T+ TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGGLDVAGQ +K++ A
Sbjct 61 LRETIQTRMNLEMAVTDEMVEIALKTQPEFVCLVPEKREELTTEGGGLDVAGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
+L +AGI+VSLFIDAD +QI AA GAP++E+HTG YADA T+ +Q EL +IA A+
Sbjct 121 HKLTEAGIKVSLFIDADRQQIDAAKACGAPYVELHTGHYADATTEEDQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL+ +VA+MK +M+
Sbjct 181 YADDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLEKSVADMKAIMVA 240

Query 241 AR 242
AR
Sbjct 241 AR 242

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>ref|ZP_01681976.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera
V52]
ref|YP_001217960.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cho
O395]
gb|EAX61205.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae
V52]
gb|ABQ21999.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae
O395]
Length=243

Score = 347 bits (889), Expect = 7e-94, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITHLREDRRRHITDRDVRI 60
M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDVRI
Sbjct 1 MSSIYLGVNIDHVATLRNARGTQYPDPVHAAEIAERAGADGITHLREDRRRHITDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGGLDV GQ ++++ A
Sbjct 61 LRETQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGGLDVLGQLERVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA
Sbjct 121 EKLTAAGIKVSLFIDADREQIDAAKACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A LG+ VNAGHGLTYHNV AIAAIP++ELNIGHAIIGRAV GL AV++MK +M+
Sbjct 181 YAHDLGITVNAGHGLTYHNVAAIAAIPAIYELNIGHAIIGRAVFDGLAKAVSDMKAIMVA 240

Query 241 AR 242
AR
Sbjct 241 AR 242

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>ref|ZP_01949430.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae
V52]

1587]
gb|EAY34143.1| pyridoxal phosphate biosynthetic protein PdxJ [*Vibrio cholerae*
 1587]
 Length=243

Score = 345 bits (886), Expect = 1e-93, Method: Compositional matrix adjust.
 Identities = 171/242 (70%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI	
Sbjct	1	MSSIY LGVNIDHVATLRNARGTQYPDPVHAAEIAERAGADGITIHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDV GQ ++++ A	
Sbjct	61	LRET LQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGLDVLGQLERVKAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA	
Sbjct	121	EKLTAAGIKVSLFIDADREQIDAACACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A G+ VNAGHGLTYHNV AIAAIP E++ELNIGHAIIGRAV GL AVA+MK +M+	
Sbjct	181	YAHDFGITVNAGHGLTYHNVAIAAIP EYELNIGHAIIGRAVFDGLAKAVADMKAIMVA	240
Query	241	AR 242	
		AR	
Sbjct	241	AR 242	

>**ref|YP_663265.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [*Pseudoalterom*
atlantica T6c]

gb|ABG42211.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [*Pseudoalteromon*
atlantica T6c]
 Length=245

GENE ID: 4175489 Pat1_3709 | pyridoxal phosphate biosynthetic protein PdxJ
 [*Pseudoalteromonas atlantica* T6c]

Score = 345 bits (885), Expect = 2e-93, Method: Compositional matrix adjust.
 Identities = 169/243 (69%), Positives = 200/243 (82%), Gaps = 0/243 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M ++LLGVNIDHIATLRNARGT+YPDPV AA IAE+AGADGIT+HLREDRRHIT DRDV +	
Sbjct	1	MRDILLGVNIDHIATLRNARGTSYPDPVHAADIAERAGADGITIHLREDRRHIMDRDVAL	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LRQT++TR+NLEMAVT+EM+ IA+ T+P FCCLVPEKR+E+TTEGGLDV G + K+ DAC	
Sbjct	61	LRQTLNTRLNLEMAVTDEMVEIALNTQPEFCCLVPEKREELTTEGGLDVVGNNQKQIADAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		K+L+DAGI VSLFIDAD QI AA AP+IEIHTG YA+AK +AEQ ELA++	
Sbjct	121	KQLSDAGILVSLFIDADFAQIDAACVACNAPYIEIHTGQYAEAKNEAEQAEALAKLVAGIE	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A + GLKVNAGHGL YHNVK IAAI ++ ELNIGHAI RA GL AV++M+ LMLE	
Sbjct	181	YADAKGLKVNAGHGLHYHNVKPIAAIKQIIELNIGHAI IARAAFDGLDKAVSDMRSLMLE	240
Query	241	ARG 243	
		AR	
Sbjct	241	ARS 243	

>**ref|ZP_03354955.1|** pyridoxal phosphate biosynthetic protein PdxJ [*Salmonella* en
 subsp. *enterica* serovar Typhi str. E01-6750]
 Length=184

Score = 343 bits (881), Expect = 6e-93, Method: Compositional matrix adjust.
 Identities = 169/184 (91%), Positives = 176/184 (95%), Gaps = 0/184 (0%)

Query	60	ILRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDA	119
		+LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDA	
Sbjct	1	MLRQTLHTRMNLEMAVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDA	60
Query	120	CKRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAA	179
		C RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGCIY+A+TDAEQ+ELARIA AA	
Sbjct	61	CARLAAAGIQVSLFIDADERQINAAAEVGAFFIEIHTGCIYANAETDAEQAKELARIASAA	120
Query	180	TFAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLML	239

```

Sbjct 121 T AA LGLKVNAGHGLTYHNVKAI AA+PEMHENLIGHAIIGRAVMTGLK+AVAEMKRLML 180
          TLAARLGLKVNAGHGLTYHNVKAI AALPEMHENLIGHAIIGRAVMTGLKEAVAEMKRLML
Query 240 EARG 243
          EARG
Sbjct 181 EARG 184

```

>ref|ZP_01898798.1| pyridoxal phosphate biosynthetic protein [Moritella sp. PE36
gb|EDM66702.1| pyridoxal phosphate biosynthetic protein [Moritella sp. PE36]
Length=245

Score = 343 bits (880), Expect = 7e-93, Method: Compositional matrix adjust.
Identities = 167/242 (69%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
        M ++ LGVNIDHIATLR ARG T YDPDV AA +AE GADGITVHLREDRRHI DRDVR+
Sbjct 1 MNKIFLGVNIDHIATLRQARGTTYDPVHAAVAELNGADGITVHLREDRRHIQDRDVRV 60

Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
        L++T+ TRMNLEMAVT EML IA E KP F CLVPEKR+E+TTEGGLDV GQ+DK+ A
Sbjct 61 LKETIQTRMNLEMAVTAEMLDIACEIKPEFVCLVPEKREELTTEGGLDVLGQQDKITQAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
        KRL++AGI VSLFIDAD+EQI AA GAP+IE+HTG YADA+++ EQ EL +IA +
Sbjct 121 KRLSEAGILVSLFIDADKEQIDAAVASGAPYIEVHTGAYADAEESEGEQQAELKKIAAGVS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
        +A + GLKVNAGHGL YHNV+ IAAIPE++ELNIGHAI I RA GL AV +M+ +M E
Sbjct 181 YAHNAGLKVNAGHGLHYHNVQPIAAIPEIYELNIGHAI IARA AFDGLGKAVKDMQVIMQE 240

Query 241 AR 242
        AR
Sbjct 241 AR 242

```

>ref|ZP_03347562.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en
subsp. enterica serovar Typhi str. E00-7866]
Length=179

Score = 340 bits (872), Expect = 6e-92, Method: Compositional matrix adjust.
Identities = 168/179 (93%), Positives = 172/179 (96%), Gaps = 0/179 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
        MAELLLGVNIDHIATLRNARGT YDPDVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTDYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
        LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC
Sbjct 61 LRQTLHTRMNLEMAVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAA 179
        RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGCIY A+A+TDAEQ A+ELARIA AA
Sbjct 121 ARLAAAGIQVSLFIDADERQINAAAEVGAFFIEIHTGCIYANAETDAEQAKELARIASAA 179

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>ref|ZP_01614216.1| pyridoxal phosphate biosynthetic protein [Alteromonadales ba
TW-7]
gb|EAW26571.1| pyridoxal phosphate biosynthetic protein [Alteromonadales bacter
TW-7]
Length=243

Score = 339 bits (869), Expect = 1e-91, Method: Compositional matrix adjust.
Identities = 162/242 (66%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
        M ++LLGVN+DHIATLR ARG T YDPD AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MKDILLGVNVDHIATLRQARGTTYDPHAHAASVAEHAGADGITIHLREDRRHIQDRDVYV 60

Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
        + +T+ TRMNLE AVT+EM+AIA+E KP + CLVPEKR+E+TTEGGLDVAG +K++ A
Sbjct 61 MAKTIQTRMNLETAVTDEMIAIALEV KPEYVCLVPEKREELTTEGGLDVAGNIEKIKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
        K L DAGI+VSLFIDAD Q+ AA GAP++EIHTG YADA D++ ++EL I +
Sbjct 121 KTLTDAGIKVSLFIDADTAQLDAAKACGAPYVEIHTGAYADATNDSDSLSELEHIRQGVQ 180

Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
        +AASLGL VNAGHGL YHNVK IAA+PE++ELNIGHAI I RA + GL AV +MKRLM+E
Sbjct 181 YAASLGLIVNAGHGLNYHNVKPIAAMPEIYELNIGHAI IARA AIDGLDKAVRDMKRLMIE 240

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Query 241 AR 242
 AR
 Sbjct 241 AR 242

>ref|ZP_01450587.1| pyridoxal phosphate biosynthetic protein [alpha proteobacter HTCC2255]
 ref|ZP_03561535.1| pyridoxine 5'-phosphate synthase [Glaciecola sp. HTCC2999]
 Length=254


Score = 338 bits (866), Expect = 3e-91, Method: Compositional matrix adjust.
 Identities = 168/240 (70%), Positives = 196/240 (81%), Gaps = 0/240 (0%)


Query 3 ELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILR 62
 E+LLGVNIDH+ATLRNARGT+YPDPV AA IAE+AGADGITVHLREDRRHI DRDV IL
 Sbjct 6 EVLLGVNIDHVATLRNARGTSYPDPVHAADIAERAGADGITVHLREDRRRHINDRDVEILA 65

Query 63 QTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDACKR 122
 +TL+TRMNLEMAVT+EMLAIA +T+P FCCLVPEKR E+TTEGGL+VAG +M+DAC +
 Sbjct 66 RTLNTRMNLEMAVTDEMLAIAKKTQPAFCCLVPEKRAELTTEGGLNVAGNLSRMQDACGQ 125

Query 123 LADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAATFA 182
 LA+ GI VSLFIDA+ EQI AA P+IEIHTG YADA + +Q QELA++ FA
 Sbjct 126 LAEQGILVSLFIDAEPEQIDAACVADVPYIEIHTGQYADATSIKQQTQELAKLKAGIQFA 185

Query 183 ASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEAR 242
 GL+VNAGHGL YHNVK IAAIPE+ ELNIGHAI+ RA+ GL AV++M+ LM EAR
 Sbjct 186 HQRGLQVNAGHGLHYHNVKPIAAIPEIVELNIGHAIMARAMFDGLGKAVSDMRALMQEAR 245

>ref|YP_563765.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shewanella de OS217]

gb|ABE56042.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shewanella deni OS217]
 Length=245

GENE ID: 4019282 Sden_2763 | pyridoxal phosphate biosynthetic protein PdxJ
 [Shewanella denitrificans OS217]

Score = 335 bits (860), Expect = 1e-90, Method: Compositional matrix adjust.
 Identities = 174/242 (71%), Positives = 197/242 (81%), Gaps = 0/242 (0%)


Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
 M+ +LLG+NIDHIATLR ARG T YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
 Sbjct 1 MSGILLGINIDHIATLRQARGTNYPDPVHAAVAEHAGADGITIHLREDRRRHIIIDRDVYL 60


Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
 L +TL TRMN E AVTEEM+AIA + KP + CLVPEKR+E+TTEGGLDVAGQ DK+ A
 Sbjct 61 LAKTLKTRMNFEEFAVTEEMIAIACDVKPAYACLVPEKREELTTEGGLDVAGQMDKITA AV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
 RLA GI+VSLFIDAD QI AA GAP+IEIHTGCIYADAK D+EQ A EL RI K A
 Sbjct 121 SRLAAHGIKVSLFIDADATQIDA AVATGAPYIEIHTGCIYADAKNDSEQAMELERITKMAK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
 +A S GL VNAGHGL YHNVKAIAAIP++ELNIGHA+I RA + GL+ AV +MKRLMLE
 Sbjct 181 YAHSGKLVVNAGHGLHYHNVKAIAAIPELYELNIGHAVIARA AIDGLETAVRDMKRLMLE 240

Query 241 AR 242
 R
 Sbjct 241 GR 242

>ref|YP_001553716.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS195]

gb|ABX48456.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS195]
 Length=245

GENE ID: 5753009 Sbal195_1281 | pyridoxal phosphate biosynthetic protein PdxJ
 [Shewanella baltica OS195]

Score = 335 bits (859), Expect = 2e-90, Method: Compositional matrix adjust.
 Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60

```

Sbjct 1      M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
MSRILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL 60

Query 61      LRQTLDTMRNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct 61      LAKTLKTRMNFECVTEEMLNIAACEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITS AV 120

Query 121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A
Sbjct 121     TRLAAGEIQVSLFIDADKTQIDAASVAGAPLIEIHTGCIYADAKTEAEEATELARISEMAK 180

Query 181     FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181     YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLMLLE 240

Query 241     AR 242
R
Sbjct 241     GR 242

```

>ref|YP_270774.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psy 34H]

sp|Q47WP8.1|PDXJ COLP3 **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short= gb|AAZ25393.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psych 34H]
Length=246

GENE ID: 3519304 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psychrerythraea 34H] (10 or fewer PubMed links)

Score = 335 bits (859), Expect = 2e-90, Method: Compositional matrix adjust.
Identities = 167/242 (69%), Positives = 192/242 (79%), Gaps = 0/242 (0%)

```

Query 1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
M+ELLLGVN+DHIATLR ARG+YPDPV AA +AE AGADGITVHLREDRRHI DRD+ +
Sbjct 1      MSELLLLGVNVNDHIATLRQARGTNYDPVYAASVAEHAGADGITVHLREDRRHIQDRDIHV 60

Query 61      LRQTLDTMRNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
L+QTL TRMN EMV+T+EM+AIA + KP FCCLVPEKR+E+TTEGGLDV GQ DK+ A
Sbjct 61      LKQTLHTRMNFEMAVTDEMIACDVKPVFCCLVPEKREELTTEGGLDVVGQLDKITKAT 120

Query 121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
++L AGI VSLFIDAD+ QI AA AP+IEIHTG YAD ++ EQ EL R+
Sbjct 121     EQLTAAGIAVSLFIDADKAQIDAASVASKAPYIEIHTGHYADLSSEEEQLIELERLTVGIK 180

Query 181     FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A +LGLKVNAGHGL Y NVK IAAI E+ ELNIGHAI RA + GL AV +MK+LMLE
Sbjct 181     YAHNLGLKVNAGHGLNYFNVKPIAAIKEIIELNIGHAIIARAAIDGLDKAVRDMKQLMLE 240

Query 241     AR 242
AR
Sbjct 241     AR 242

```

>ref|YP_734973.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp MR-4]

gb|ABI39916.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-4]
Length=245

GENE ID: 4253416 **Shewmr4_2845** | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-4]

Score = 335 bits (858), Expect = 3e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1      MSRILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL 60

Query 61      LRQTLDTMRNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct 61      LAKTLKTRMNFECVTEEMLNIACEVKTPTVCLVPEKRQEVTTTEGGLDVAGQLDKITAAV 120

Query 121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
RLA GIQVSLFIDAD+ QI AA E GAP IEIHTGCIYADAKT E+A+ELARI++ A

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```

Sbjct 121 SRLAANGIQVSLFIDADKTQIDAAVESGAPLIEIHTGCIYADAKTAEAAEAKELARISEMAK 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIIPPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE 240
Query 241 AR 242
      R
Sbjct 241 GR 242

```

>ref|YP_339261.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromonas haloplanktis TAC125]

sp|Q3IDK9.1|PDXJ PSEHT **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=emb|CAI85818.1| **G** pyridoxine 5'-phosphate (PNP) synthase [Pseudoalteromonas haloplanktis TAC125]
Length=243

• GENE ID: 3709965 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromonas haloplanktis TAC125] (10 or fewer PubMed links)

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 161/242 (66%), Positives = 195/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRRHITDRDVRI 60
      M ++LLGVN+DHIATLR ARG+YPDP AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MKDILLGVNVDHIATLRQARGTSYPDPAHAASVAEHAGADGITIHLREDRRHIQDRDVYV 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQEVTTTEGGLDVAGQDRDKMRDAC 120
      + +T+ TRMNLE AVT+EM+ IA+E KP + CLVPEKR+E+TTEGGLDVAG +K+ A
Sbjct 61 MAKTIQTRMNLETAVTDEMINIALEVKPEYVCLVPEKREELTTEGGLDVAGNLEKITAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      K L+DAGI+VSLFIDAD+ Q+ AA GAP++EIHTG YADA TD ++EL I +
Sbjct 121 KTLSDAGIKVSLFIDADKAQLDAAKATGAPYVEIHTGAYADATTDEAISKELEHIRQGVK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +AAS+GL VNAGHGL YHNVK IAA+ E++ELNIGHAI RA + GL AV +MKRLMLE
Sbjct 181 YAASIGLIVNAGHGLHYHNVKPIAAEETIYELNIGHAIARAAIDGLDKAVRDMKRLMLE 240

Query 241 AR 242
      AR
Sbjct 241 AR 242

```

>ref|YP_002359017.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS223]

gb|ACK47594.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS223]
Length=245

GENE ID: 7087887 **Sba1223_3109** | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS223]

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRRHITDRDVRI 60
      M+ ++LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQEVTTTEGGLDVAGQDRDKMRDAC 120
      L +TL TRMN E AVTEEM LA E KP + CLVPEKQEVTTTEGGLDVAGQ DK+ A
Sbjct 61 LAKTLKTRMNFECVTEEMLNIAICEIKPTYVCLVPEKQEVTTTEGGLDVAGQLDKITA AV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A
Sbjct 121 TRLAAEGIQVSLFIDADKTQIDAABAAGAPLIEIHTGCIYADAKTEAEEATELARISEMAK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLMLLE 240

Query 241 AR 242
      R
Sbjct 241 GR 242

```

>ref|YP_001365462.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS185]

gb|ABS07399.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS185]
Length=245

GENE ID: 5372257 Shew185_1248 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS185]

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Sbjct	1	MSRILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL	60
Query	61	LRQTL DTRMNLEMAVTEEMLAI AVETKPHFCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
		L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A	
Sbjct	61	LAKTLKTRMNFECVTEEMLNIACEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITA AV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A	
Sbjct	121	TRLAAEGIQVSLFIDADKTQIDA AVASGAPLIEIHTGCIYADAKTEAEAEELARISEMAK	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE	
Sbjct	181	YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVMLE	240
Query	241	AR 242	
		R	
Sbjct	241	GR 242	

>ref|YP_001182689.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella CN-32]

gb|ABP74890.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putr CN-32]
Length=245

GENE ID: 5081572 Sputcn32_1162 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putrefaciens CN-32]

Score = 333 bits (854), Expect = 8e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Sbjct	1	MSRILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL	60
Query	61	LRQTL DTRMNLEMAVTEEMLAI AVETKPHFCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
		L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A	
Sbjct	61	LAKTLKTRMNFECVTEEMLNIACEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITA AV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A	
Sbjct	121	TRLAAEGIQVSLFIDADKTQIDA AVASGAPLIEIHTGCIYADAKTEAEAEIELARISEMAK	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE	
Sbjct	181	YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE	240
Query	241	AR 242	
		R	
Sbjct	241	GR 242	

>ref|YP_001049591.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS155]

gb|ABN60722.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS155]
Length=245

GENE ID: 4842456 Sbal_1204 | pyridoxal phosphate biosynthetic protein PdxJ

[Shewanella baltica OS155]

Score = 333 bits (853), Expect = 8e-90, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAAVAHAAGADGITIHLREDRRHIIDRDVYL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQDKMRDAC 120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKROEVTTEGGGLDVAGQ DK+ A
Sbjct 61  LAKTLKTRMNFECVTEEMLNIAICEIKPTYVCLVPEKROEVTTEGGGLDVAGQDKITAAY 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+A++A ELARI++ A
Sbjct 121  TRLAAGIQVSLFIDADKTQIDAASVAGAPLIEIHTGCIYADAKTEAQEATELARISEMAK 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLMLLE 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>ref|YP_001500902.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella ATCC 700345]

gb|ABV86367.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella peal ATCC 700345]
 Length=245

GENE ID: 5661439 Spea 1040 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella pealeana ATCC 700345]

Score = 332 bits (852), Expect = 1e-89, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGA+GIT+HLREDRRHI DRDV
Sbjct 1  MSRIILLGVNIDHIATLRQARGTNYPDPVHAAAVAHAAGAEGITIHLREDRRHIIDRDVYT 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQDKMRDAC 120
          L +TL TRMN EMVTEEML IA E KP + CLVPEKR+E+TTEGGGLDVAGQ+DK+ A
Sbjct 61  LAKTLKTRMNFEMVTEEMLNIAICEIKPAYVCLVPEKREELTTEGGGLDVAGQDKIAAAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RL GI+VSLFIDAD QI AA VGAP IEIHTGCIYADA+TD+EQA EL RI + AT
Sbjct 121  ARLTKEGIKVSLFIDADSTQIDAASVAVGAPVIEIHTGCIYADAETDSEQAAELKRITEMAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A GL VNAGHGL YHNVKAIAAIPE++ELNIGHAII RA + GL AV +MK+LMLE
Sbjct 181  YAHGKGLVVNAGHGLHYHNVKAIAAIPELYELNIGHAIIARAAIDGLATAVRDMKQLMLE 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>ref|YP_738968.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp MR-7]

gb|ABI43911.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-7]
 Length=245

GENE ID: 4257702 Shewmr7_2927 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-7]

Score = 332 bits (851), Expect = 2e-89, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 195/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAAVAHAAGADGITIHLREDRRHIIDRDVYL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQDKMRDAC 120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKROEVTTEGGGLDVAGQ DK+ A

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Sbjct  61  LAKTLKTRMNFECVTEEMLNIAACEVKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITVAV  120
Query  121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAEQELARIAKAAT  180
          RLA  GIQVSLFIDAD+ QI AA  GAP IEIHTGCIYADAKT  E+A+ELARI++ A
Sbjct  121  SRLAANGIQVSLFIDADKTQIDAAVASGAPLIEIHTGCIYADAKTAEAAEAKELARISEMAK  180
Query  181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +A  GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL  AV +MK LMLE
Sbjct  181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE  240
Query  241  AR  242
          R
Sbjct  241  GR  242

```

>ref|YP_751604.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella fr NCIMB 400]

gb|ABI72765.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella frig NCIMB 400]
Length=265

GENE ID: 4279831 Sfri 2926 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella frigidimarina NCIMB 400]

Score = 332 bits (851), Expect = 2e-89, Method: Compositional matrix adjust.
Identities = 173/239 (72%), Positives = 196/239 (82%), Gaps = 0/239 (0%)

```

Query  4  LLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRILRQ  63
          +LLG+NIDHIATLR ARGV YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +L +
Sbjct  24  ILLGINIDHIATLRQARGTHYPDPVHAAVAEHAGADGITIHLREDRRHIQDRDVIYLLAK  83
Query  64  TLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDACKRL  123
          TL TRMN E AVTEEM+AIA + KP + CLVPEKR+E+TTEGGLDVAGQ DK+R A  RL
Sbjct  84  TLKTRMNFECVTEEMIAIACDIKPAYACLVPEKREELTTEGGLDVAGQLDKIRSAVTRL  143
Query  124  ADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAEQELARIAKAATFAA  183
          A  GI+VSLFIDAD+ QI AA  GAP+IEIHTGCIYADA TDAEQAE EL RI + A +A
Sbjct  144  AAEIGIKVSLFIDADKTQIDAAVLGAPYIEIHTGCIYADAITDAEQADELVRITEMAQYAH  203
Query  184  SLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLEAR  242
          S GL VNAGHGL YHNVKAIAAIPE++ELNIGHAI+I RA + GL  AV +MK+LMLE R
Sbjct  204  SKGLVVNAGHGLHYHNVKAIAAIPELYELNIGHAIVARAAIDGLDTAVRDMKKMLMEGR  262

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>ref|YP_964373.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp W3-18-1]

ref|ZP_01706794.1| pyridoxal phosphate biosynthetic protein PdxJ [Shewanella pu 200]

gb|ABM25819.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. W3-18-1]

gb|EAY52920.1| pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putref 200]
Length=245

GENE ID: 4661399 Sputw3181_3002 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. W3-18-1]

Score = 332 bits (850), Expect = 2e-89, Method: Compositional matrix adjust.
Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query  1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI  60
          M+ +LLGVNIDHIATLR ARGV+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct  1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL  60
Query  61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC  120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct  61  LAKTLKTRMNFECVTEEMLNIACEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITAAV  120
Query  121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAEQELARIAKAAT  180
          RLA  GIQVSLFIDAD+ QI AA  GAP IEIHTGC+ADAKT+AE+A ELARI++ A
Sbjct  121  TRLAEEGIQVSLFIDADKTQIDAAVASGAPLIEIHTGCFADAKTEAAEAEIELARISEMAK  180
Query  181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +A  GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL  AV +MK LMLE
Sbjct  181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE  240
Query  241  AR  242

```


Sbjct 241 ^RGR 242

>ref|YP_001673314.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella HAW-EB4]

gb|ABZ75655.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella hali HAW-EB4]
Length=245

GENE ID: 5904608 Shal_1086 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella halifaxensis HAW-EB4]

Score = 330 bits (845), Expect = 7e-89, Method: Compositional matrix adjust.
Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M +LLGVNIDHIATLR ARG T YDPDV AA +AE AGA+GIT+HLREDRRHI DRDV	
Sbjct	1	MGRILLGVNIDHIATLRQARGTNYPDPVHAAVAEHAGAEGITIHLEDRRRHIIDRDVYT	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC	120
		L +TL TRMN EMAVTEEM L IA + KP + CLVPEKR+E+TTEGGLDVAGQ+DK+ A	
Sbjct	61	LAKTLKTRMNFEMAVTEEMLDIACDIKPAYVCLVPEKREELTTEGGLDVAGQQDKIAAAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		RL GI+VSLFIDAD+ QI AA VGAP IEIHTGICYADA+TDAEQA EL RI + AT	
Sbjct	121	ARLTQEGIKVSLFIDADKAQIDA AVAVGAPVIEIHTGICYADAETDAEQATELQRITEMAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A GL VNAGHGL YHNVKAAIAAIP E+ELNIGHAII RA + GL AV +MK+LMLE	
Sbjct	181	YAHGKGLVVNAGHGLHYHNVKAAIAAIP ELYELNIGHAIIARAAIDGLATAVRDMKQLMLE	240
Query	241	AR 242	
		^R	
Sbjct	241	GR 242	

>ref|YP_001093187.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella PV-4]

gb|ABO22928.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella loih PV-4]
Length=245

GENE ID: 4921109 Shew_1057 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella loihica PV-4]

Score = 329 bits (844), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 200/242 (82%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M+ + LGVNIDHIATLR ARG T+YDPDV AA +AE AGA+GITVHLREDRRHI DRD+ +	
Sbjct	1	MSRIHLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGAEGITVHLREDRRHICDRDIYL	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC	120
		L +T+ TRMN EMAVT+EML IA E KP + CLVPEKR+E+TTEGGLDVAGQ+DK+R A	
Sbjct	61	LAKTIKTRMNFEMAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGLDVAGQQDKIRAAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		+RL GI+VSLFIDAD QI A VGAP IE+HTGICYADA+TDAEQA+ELARI + AT	
Sbjct	121	ERLTALGIKVSFLFIDADPVQIDATVAVGAPVIELHTGICYADAETDAEQAKELARITEMAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A GL VNAGHGL YHNVK+IAAIP E++ELNIGHAII RA + GL AV +MK+LM+E	
Sbjct	181	YAHGKGLVVNAGHGLHYHNVKSIAAIP ELYELNIGHAIIARAAIDGLKAVRDMKQLMVE	240
Query	241	AR 242	
		^R	
Sbjct	241	GR 242	

>ref|YP_001759633.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella ATCC 51908]

gb|ACA85538.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella wood ATCC 51908]
Length=245

GENE ID: 6115481 Swoo 1246 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella woodyi ATCC 51908]

Score = 329 bits (844), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 197/242 (81%), Gaps = 0/242 (0%)


```
Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGA+GITVHLREDRRHI DRD+ +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAEGITVHLREDRRHIVDRDIYL 60


Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
      L +TL TRMN EMAVT+EML IA E KP + CLVPEKR+E+TTEGGGLDVAGQ K+ A
Sbjct 61 LAKTLKTRMNFEMAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGGLDVAGQMGKIESAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      +RL D G++VSLFIDAD+ QI AA VGAP IEIHTGCIYADA DA+QA+ELARI + AT
Sbjct 121 QRLTDIGVKVSLFIDADKTQIDAABAAGAPVIEIHTGCIYADATNDADQAKELARITEMAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI RA + GL AV +MK+LM E
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIARAAIDGLATAVKDMKQMLNE 240

Query 241 AR 242
      R
Sbjct 241 GR 242
```

>ref|YP_870654.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp ANA-3]

gb|ABK49248.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. ANA-3]
Length=245

GENE ID: 4478566 Shewana3_3023 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. ANA-3]

Score = 329 bits (843), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 194/242 (80%), Gaps = 0/242 (0%)


```
Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAEGADGITIHLREDRRHIDRDVYL 60


Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
      L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGGLDVAGQ DK+ A
Sbjct 61 LAKTLKTRMNFECVTEEMLNIAICEVKPTYVCLVPEKRQEVTTTEGGGLDVAGQLDKITAAB 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      RLA IQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT E+A+ELARI++ A
Sbjct 121 SRLAANRIQVSLFIDADKTQIDAABAAGAPLIEIHTGCIYADAKTAEELAKELARISEMAK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI RA + GL AV +MK LMLE
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE 240

Query 241 AR 242
      R
Sbjct 241 GR 242
```

>ref|NP_716971.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shewanella on MR-1]

sp|Q8EH78.1|PDXJ_SHEON RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
gb|AAN54416.1|AE015579_5  pyridoxal phosphate biosynthetic protein PdxJ [Shewa MR-1]
Length=245

GENE ID: 1169172 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella oneidensis MR-1] (10 or fewer PubMed links)

Score = 328 bits (842), Expect = 2e-88, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 193/242 (79%), Gaps = 0/242 (0%)

```
Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAEGADGITIHLREDRRHIDRDVYL 60
```

```

Query   61   LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC   120
          L +TL TRMN E AVTEEM L IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct   61   LAKTLKTRMNFEC AVTEEM LNIACEVKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITAAV   120

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEV G A P F I E I H T G C Y A D A K T D A E Q A Q E L A R I A K A A T   180
          R L A G I Q V S L F I D A D + Q I A A G A P I E I H T G C Y A D A K T E + A + E L R I + A
Sbjct   121  SRLAANGIQVSLFIDADKTQIDA AVASGAPLIEIHTG CYADAKTAD EEAKELE RIREMAK   180

Query   181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
          +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct   181  YAHGKGLIVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAV KDMKTLMLE   240

Query   241  AR   242
          R
Sbjct   241  GR   242

```

>ref|YP_942095.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas 37]
gb|ABM02496.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas in 37]
 Length=244

GENE ID: 4626841 Ping_0643 | pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas ingrahamii 37]

Score = 328 bits (840), Expect = 3e-88, Method: Compositional matrix adjust.
 Identities = 162/242 (66%), Positives = 192/242 (79%), Gaps = 0/242 (0%)

```

Query   1   MAELL LGVNIDHIATLRNARGTAYPDPVQAA FIAEQAGADGITVHLREDRRHITDRDVRI   60
          M+++LLGVNIDHIATLRNARGT YP+P A IAE AGADGIT+HLREDRRHI DRDV +
Sbjct   1   MSQILLGVNIDHIATLRNARGTCYPEPAHLAAIAECAGADGITIHLREDRRHINDRDVAV   60

Query   61   LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC   120
          L QTL TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGL+V K+ A
Sbjct   61   LAQTLQTRM NLEMAVTDEMVDIALKTKPAFVCLVPEKREELTTEGGLNVVASFSKIASAV   120

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEV G A P F I E I H T G C Y A D A K T D A E Q A Q E L A R I A K A A T   180
          R L A I Q V S L F I D + Q I A A + G A + I E + H T G Y A D A ++ Q E L R + A K A A T
Sbjct   121  SRLNAAAIQVSLFIDPEN AQIDA A I K T G A A Y I E L H T G K Y A D A P S E D I Q Q F E L M R V A K A A T   180

Query   181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
          +A+ G+KVNAGHGL YHNVK IAA+PE+ ELNIGHAI+ RA++ G AVAEMKRLM+E
Sbjct   181  YASQAGIKVNAGHGLNYHNVKPIAALPEIIELNIGHAIVARALVDGFGPAVAEMKRLMVE   240

Query   241  AR   242
          R
Sbjct   241  GR   242

```

>ref|YP_693348.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax b SK2]

sp|Q0VP22.1|PDXJ ALCBS **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
emb|CAL17076.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax bo SK2]
 Length=244

GENE ID: 4212451 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax borkumensis SK2] (10 or fewer PubMed links)

Score = 328 bits (840), Expect = 3e-88, Method: Compositional matrix adjust.
 Identities = 163/238 (68%), Positives = 187/238 (78%), Gaps = 0/238 (0%)

```

Query   1   MAELL LGVNIDHIATLRNARGTAYPDPVQAA FIAEQAGADGITVHLREDRRHITDRDVRI   60
          M+ +LLGVNIDHIATLR ARG T YP+PVQAA +AEQAGADGITVHLREDRRHI DRDV +
Sbjct   4   MSRVLLGVNIDHIATLRQARGTRYPEPVQAALVAEQAGADGITVHLREDRRHINDRDVEL   63

Query   61   LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC   120
          L QTL TRMNLEMA TEEM+ IA +P CCLVPEKR+E+TTEGGLDV G + + C
Sbjct   64   LAQTLQTRM NLEMAATEEMVVIACRIQPPHCCLVPEKREELTTEGGLDVVGNKAWIAQCC   123

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEV G A P F I E I H T G C Y A D A K T D A E Q A Q E L A R I A K A A T   180
          +R L A G I +V S L F I D A +E Q I A A E G A P I E I H T G Y A D A +T +Q Q E L A R I A
Sbjct   124  QRLGQAGIEVSLFIDAEESQILAARECGAPAIEIHTGGYADAQTIDQQQQELARIRSAVA   183

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Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLM	238
		FA + GL VNAGHGL YHN AIA IP ++ELNIGH+II RA +TGL +AV M+ L+	
Sbjct	184	FALAQGLIVNAGHGLHYHNTLAIAEIPGINELNIGHSSIARAATGLDEAVRSMRSL	241

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